

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number

TO: Nita M Minnifield

Location: REM/3C01/3C18

Art Unit: 1645

Saturday, September 17, 2005

Case Serial Number: 10/002784

From: Edward Hart

Location: Biotech-Chem Library

REM-1A55

Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Minnifield,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

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From:

Minnifield, Nita

Sent:

Thursday, September 15, 2005 4:51 PM

To: Subject: STIC-Biotech/ChemLib sequence search

10/002784

STIC

Please do a commercial and interference sequence search on SEQ ID NO:16 and 27 of this application.

Please provide a paper copy of all results.

Thanks,
Minnifield
71976
Art Unit 1645
Office REM-3C01
Mailbox REM-3C18
571-272-0860

RECEIVED

SEP 15 2008

*TECH/CHEM. DIVISION

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
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                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
enterotoxin B at 1.5-A resolution: implications for superantigen recognition by MHC class II molecules and T-cell receptors."; J. MOL. Biol. 277:61-79(1998).
-!- FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases
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DQFLYFDLI -> NEFFDLIXL (in Ref. 3).

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R InterPro; IPR008992; Bact endotox.
R InterPro; IPR006123; Staph/Strept tox.
R InterPro; IPR006123; Staph/Strept tox.
R InterPro; IPR006124; Staph tox OB.
R InterPro; IPR006125; Staph tox OB.
R InterPro; IPR006175; Staph tox OB.
R Pfam; PF01203; Stap Strp_tox.
R Pfam; PF01213; Stap Strp_tox.
R PRIMTS; PR00279; BACTRITOXIN.
R PROSITE; PS00279; STAPH STREP_TOXIN.
R PROSITE; PS00278; STAPH STREP_TOXIN.
R PROSITE; PS00278; STAPH STREP_TOXIN.
R SUPERINGER: Direct protein Sequencing; Enterotoxin; Signal;
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PDB; 1D5X; X-ray; C=28-266.
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PDB; 1D5Z; X-ray; C=28-266.
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MEDLINE=99096298; PubMed=9881971; DOI=10.1016/S1074-7613(00)80646-9;
Li H., Llera A., Tsuchiya D., Leder L., Ysern X., Schlievert P.M.,
Karjahainen K., Mariuza R.A.;
"Three-dimensional structure of the complex between a T cell receptor
beta chain and the superantigen staphylococcal enterotoxin B.";
immunity 9:807-816(1998).
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Swaminachan S., Furey W.F. Jr., Pletcher J., Sax M.;
"Crystal structure of staphylococcal enterotoxin B, a superantigen.";
Nature 359:801-806(1992).
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Jardetzky T.S., Brown J.H., Gorga J.C., Stern L.J., Urban R.G.,
Chi Y.I., Stauffacher C., Strominger J.L., Wiley D.C.;
"Three-dimensional structure of a human class II histocompatibility
molecule complexed with superantigen.";
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Jones C.L., Khan S.A.;
"Nucleotide sequence of the enterotoxin B gene from Staphylococcus
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MEDLINE-98181012; Pubmed=9514739; DOI=10.1006/jmbi.1997.1577;
Papageorgiou A.C., Transer H.S., Acharya K.R.;
"Crystal structure of microbial superantigen staphylococcal
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Huang I.-Y., Bergdoll M.S.;
"The primary structure of staphylococcal enterotoxin B.
cyanogen bromide peptides of reduced and aminoethylated
and the complete amino acid sequence.";
J. Biol. Chem. 245:3518-3525(1970).
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MEDLINE=65298255; PubMed=3898073;
Manelli D.M., Jones C.L., Johns M.B., Mussey G.J.,
"Molecular cloning of staphylococcal enterotoxin B
coli and Staphylococcus aureus.";
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MEDLINE=99137798; PubMed=9952369;

Bessen D.E., Izzo M.W., Florentino T.R., Caringal R.M.,

A Hollingshead S.K., Beall B.;

"Genetic linkage of exotoxin alleles and emm gene markers for tissue
Troplsm in group A streptococci.";

"Infect. Dis. 179:627-636(1999).

EMBL, AFC190951; AAD21315.1; -.

R HSSP, PO1552; 1SEB.

GO: GO:0009405; P: pathogenesis; IEA.

R O: GO:0009405; P: pathogenesis; IEA.

InterPro; IPR006123; Stap/Strep_toxin.

InterPro; IPR006123; Stap/Strep_toxin.

InterPro; IPR006123; Stap/Strep_toxin.

R InterPro; IPR006123; Stap/Strep_toxin.

R InterPro; IPR006173; Staph/Strep_toxin.

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R InterPro; IPR006123; Staph/Strep_toxin.

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Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
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25884 MW; 121F8460992818F8 CRC64;
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                                                                             39.3%; Score 981.5; DB 2; ilarity 87.7%; Pred. No. 1.3e-55; Conservative 13; Mismatches 12;
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87.7%; Pred. No. 1.3e-55;
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                                                                                Query Match
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NCBI_TaxID=119602;
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Q938P4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 ELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHDLIYNVSGPNYDKLKT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;

"Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogens.",

J. Exp. Med. 174:L271-L274(1991).

EMBL; X61573; CA443771.1;

EMBL; X61573; CA43771.1;

HSSP; P01522; 188B.

GO, GO:0005576; C:extracellular; IEA.

GO, GO:0009405; P:pathogenesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 VSIDGIQSLSFDIETNKKAAVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE
                                                the speA
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A Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;

"Characterization and clonal distribution of four alleles of the gree encoding pyrogenic exotoxin A (scarlet fever toxin) in Strepencoccus pyrogenic exotoxin A (scarlet fever toxin) in Strepencoccus pyrogenes.";

J. Exp. Med. 174:1271-1274(1991).

B. Rabi, Kel554; C. Caxtracellular; IEA.

GO; GO:0005405; P:pathogenesis; IEA.

R. TherPro; IPR006137; Bath_Cox.

R. InterPro; IPR006123; Stap_Strep_toxin.

R. InterPro; IPR006123; Stap_Strep_toxin.

R. InterPro; IPR006123; Stap_Strp_tox_OB.

Pfam; PF01123; Stap_Strp_tox_OB.

Pfam; PF01123; Stap_Strp_tox_C; 1.

R. RINTS; PR00275; BATHERTJÖXIN.

R. RINTS; PR00277; STAPH_STREP_TOXIN_1; 1.

R. RINTS; PR00277; STAPH_STREP_TOXIN_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.1%; Score 1027.5; DB 2; Length
98.0%; Pred. No. 1.4e-58;
tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 1 Potential.
23 >220 type A exotoxin.
220 220 WW, 92DB096E57906DF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 AA
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MEDLINE=92044323; PubMed=1940804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203 SFWFDFFPEPEFTQSKYL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 SFWFDFFPEPEFTQSKYL 198
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Best Local Similarity 98.0
Matches 194; Conservative
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NCBI_TaxID=1314;
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Q54696
                셤
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ELKOQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 VSIDGIQSLSFDIETSKKMVTAQELDYKVRKHLTDNKQLYTNGPSKYETGYIKFISKDKE 202
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XA Malia A., Bessen D. B.;

Kalia A., Bessen D. B.;

YET BESSEN BESSEN D. B.;

Presence of streptococcal pyrogenic exotoxin A and C genes in human isolates of group G streptococci.";

FMS Microbiol. Lett. 219:291-295 (2003).

REMBL, AY049745; AAL06068.1; -.

REMBL, AY049745; AAL06068.1; -.

RO, GO.0005576; C: extracellular; IEA.

GO, GO.0005576; C: extracellular; IEA.

GO, GO.0005576; C: extracellular; IEA.

RO, GO.0009405; P:pathogenesis; IEA.

InterPro; IPR006127; Stap. Lox.

InterPro; IPR006128; Staph/Strept.tox.

InterPro; IPR006129; Staph/Strept.tox.

InterPro; IPR006179; Staph tox.

Ros Pro; IPR006179; Staph tox.

Ros Pro; RR00279; Staph tox.

REMM; PF01123; Stap Strp.toxin; 1.

REMM; PR02171; STAPH STREP TOXIN 1; 1.

RROSITE; PS00277; STAPH STREP TOXIN 2; 1.

RON_TER.

NON_TER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.5%; Score 986.5; DB 2; Length 88.2%; Pred. No. 6.9e-56; Live 13; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                             1 1 Potential.
23 >236 type A exotoxin.
236 236 Type A exotoxin.
236 AA; 27575 MW; 70F54120E79127DF CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 SFWFDFFPEPEFTQSKYLMIYKDNETLDSNT 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 TFWFDFFPEPEFNQVKYLMIYKDNETLDSST 233
InterPro; IPR008992; Bact_endotox.
InterPro; IPR006177; Bctrl_tox.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006126; Staph/Strep_toxin.
InterPro; IPR006126; Staph/Strep_tox.
InterPro; IPR006173; Staph tox OB.
Pfam; PF01123; Stap Strp_toxin; 1.
Pfam; PF02176; Stap Strp_toxin; 1.
PR0SITE; PS00277; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyrogenic exotoxin A (Fragment).
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ELKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 QQDPDFSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHDLIYNVSGPNYDKLYT
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                   MEDLINE-92044323; PubMed=1940804;

MEDLINE-92044323; PubMed=1940804;

Melson K., Schlievert P.M., Selander R.K., Musser J.M.;

"Characterization and clonal distribution of four alleles of the gene encoding pyrogenic exotoxin A (scarlet fever toxin) in J. Exp. Med. 1741271-1274(1991).

BMEL; X61562; CAA43760.1; -...

BMEL; X61563; CAA43760.1; -...

BMEL; X61564; CAA43762.1; -...

BMEL; X61565; CAA43762.1; -...

BMEL; X61565; CAA43762.1; -...

BMEL; X61565; CAA43763.1; -...

BMEL; X6108; A60108; A60108.1; A60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.6%; Score 1089.5; DB 2; Length
97.6%; Pred. No. 1.6e-62;
ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pyogenes.
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 1 22 Potential.
23 >236 type A exotoxin.
236 236 236 WW; 2EF7F41AAC853600 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Type A exotoxin precursor (Fragment).
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STRAIN-MGAS500;
MEDLINE-92044323; PubMed=1940804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 206; Conservative
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NCBI_TaxID=1314;
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SEQUENCE
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SIGNAL
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Q79AQ0;
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      RAY KARATA KARAK K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 ELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 VSIDGIQSLSFDIETNKGMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 VSIDGIQSLSFDIETNKKAVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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                                                                                                                                                                  вред
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                SEQUENCE FROM N.A.

STRAIN=MGAS165, MGAS327, MGAS493, MGAS167, and MGAS156;

KEDLINE=92044322, PubMed=1940804,

NeDLINE=92044322, PubMed=1940804,

Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;

"Characterization and clonal distribution of four alleles of the spence encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.", Streptococcus pyogenes.",
                                                                                                                                                              the
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SEQUENCE FROM N.A.
STRAIN=MGAS156, MGAS256, MGAS285, MGAS480, MGAS492, and
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43.8%; Score 1095.5; DB 2; Length 236;
Best Local Similarity 98.1%; Pred. No. 6.4e-63;
Matches 207; Conservative 1; Mismatches 2; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27454 MW; 3FB3F41ABDC13A84 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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type A exotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact endotox.
InterPro; IPR008912; Bat Endotox.
InterPro; IPR006123; Stap/Strept tox.
InterPro; IPR006126; Staph/Strept tox.
InterPro; IPR006126; Staph/Strept tox.
Pfam; PF01123; Stap_Strp_tox.
Pfam; PF01123; Stap_Strp_tox.
INTERPRO; IPR005179; BACTRITOXIN.
PROSITE; PS00277; STAPH_STREP_TOXIN 1; IPROSITE; PS00277; STAPH_STREP_TOXIN 1; IPROSITE; PS002778; STAPH_STREP_TOXIN 1; IPROSITE; PS002778; STAPH_STREP_TOXIN 2; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 SFWFDFFPEPEFTQSKYLMIYKONETLDSNT 233
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Name=speA;
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<1
23 >2
236 2
236 AA;
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NCBI_TaxID=1314;
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01-MAY-2000 (
01-OCT-2003 (
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STRAIN=MGAS485, MGAS491, MGAS495, and MGAS624;

MEDLINE=92044323; PubMed=1940804;

MEDLINE=92044323; PubMed=1940804;

Melson K., Schlievert P.M., Schlader R.K., Musser J.M.;

"Characterization and clonal distribution of four alleles of the speat gene encoding pyrogenic exotoxin A (scarlet fever toxin) in 5 gene encoding pyrogenes ";

"Streptococcus pyogenes";

"Streptococcus pyogenes";

"A Streptococcus pyogenes";

"A Streptococcus pyogenes";

"B EMBL; X61569; CAA43767.1;

"B EMBL; X61569; CAA43769.1;

"R EMBL; X61570; CAA43769.1;

"R EMBL; X61571; CAA43769.1;

"R EMBL; X61088; A60108.

"R HSSP; P01552; 155B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 QQDPDPSQLHRSSLVKKLQNIYFLYEGDPVTHENVKSVDQLLSHDLIYNVSGPNYDKLKT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKT
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43.9%; Score 1096.5; DB 2; Length
Best Local Similarity 98.6%; Pred. No. 5.5e-63;
Matches 208; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pyogenes.
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
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>236 type A exotoxin.
236
; 27468 MW; 29DF2AD575623A84 CRC64;
                                                                                                                                                              054779; Q54613; Q54736; Q54740; Q54741; Q54779; Q54779; Q54771; Qreated (TrEMBLE). 01. Last sequence update) 05-JUL-2004 (TrEMBLE). 27, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFWFDFFPEFFTQSKYLMIYKDNETLDSNT 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact_endotox.
InterPro; IPR008912; Bact_andotox.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006126; Staph/Strept_tox.
InterPro; IPR006173; Staph.tox_OB.
Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF02876; Stap_Strp_toxin; 1.
PROSITE; PS00277; STAPH_STREP_TOXIN 1; 1.
PROSITE; PS00277; STAPH_STREP_TOXIN 1; 1.
                                                                                                                                                                                                                                                                                                              Type A exotoxin precursor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus.
NCBI_TaxID=1314;
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SIGNAL
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                                                    RESULT 7
Q54779
                                                                                                                                        ALL BELLE SOLO BELLE SELLE SEL
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RESULT 8 Q9R931

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ELKNOEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTWREGNHLEIPKKIVVK 120
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MEDLINE-99137798; PubMed=9952369;

MEDLINE-99137798; PubMed=9952369;

MEDLINE-99137798; PubMed=9952369;

MEDLINE-99137798; PubMed=9952369;

MEDLINE-99137798; M.W., Fiorentino T.R., Caringal R.M.,

MEDLINE-99137798; M.W., Piorentino T.R., Caringal R.M.,

MEDLINE-99137798; M.W., Piorentino T.R., Caringal R.M.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
43.8%; Score 1095.5; DB 2; Length
Best Local Similarity 98.1%; Pred. No. 5.9e-63;
Matches 207; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pyogenes.
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus
NCBI_TaxID=1314;
                                                                                                                                                                                                               Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 AA; 25759 MW; 48BB7ADDCD91FBA3 CRC64;
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1-MXY-1997 (TrEMBLrel. 03, Created)

01-MXY-1997 (TrEMBLrel. 03, Last sequence update)

05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                Last sequence update)
Last annotation update)
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        Created)
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Type A exotoxin precursor (Fragment)
01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25, Exotoxin A (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                        Streptococcus
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P97163
ID P971163
AC P9711
AC P9711
DT 01-M
DT 05-J
DE TYPE
CS STREE
CC BACK
OC BACK
OX NCBLE
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ODRAN SOLITARIA DE LA CONTROL 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: Causative agent of the symptoms associated with scarlet fever, have been associated with streptococcal toxic shock-like disease and may play a role in the early events of rheumatic
                                                                                  SPEA STRPY STANDARD; FRI, COLONDARD; PASSEO: P08095; 01-AUG-1998 (Rel. 08, Created) 01-JAN.1990 (Rel. 13, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Binds to major histocompatibility complex class II beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- MISCELLANEOUS: This toxin seems to be coded by bacteriophage T12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).
MEDLINE=99094887; PubMed=9878045; DOI=10.1093/emboj/18.1.9;
Papageorgiou A.C., Collins C.M., Guman D.M., Kline J.B.,
O'Brien S.M., Tranter H.S., Acharya K.R.;
"Structural basis for the recognition of superantigen streptococcal pyrogenic exotoxin A (SpeAl) by MHC class II molecules and T-cell EMBO J. 18:9-21(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=86284313; PubMed=3526093;
Johnson L.P., L'Italien J.J., Schlievert P.M.;
Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to Staphylococcus aureus enterotoxin B.";
Mol. Gen. Genet. 203:354-356(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
                                                                                                                                                                                                                                                                                                                                                                                 [1] ZEQUENCE FROM N.A. MEDIANE-86166804; PubMed=3514452; MEDIANE=86166804; PubMed=3514452; Weeks C.R., Ferretti J.J.; "Nucleotide sequence of the type A streptococcal exotoxin"
                                                                                                                                                                                                                                                                                Streptococcus pyogenes.
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR006177; BctrI_tox.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006126; Staph/Strept_tox.
InterPro; IPR006127; Staph_tox_OB.
Pfam; PF02876; Stap_Strp_tox_C, I.
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InterPro; IPR006177; Bctrī tox.
InterPro; IPR006123; Stap/Strep_to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Infect. Immun. 52:144-150(1986)
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EMBL; X03929; CAA27568.1; --
FUR; A26152; A26152.
FDB; 1B1Z; X-ray; --
FDB; 1FNU; X-ray; --
FDB; 1FNU; X-ray; --
FDB; 1FNU; X-ray; --
FDB; 1FNU; X-ray; --
FDB; 1FNY; X-ray; --
FDB; 1FNS; X-ray; --
FDB; 1HAS; X-ray; --
FDB; 1HAS; X-ray; --
                                                                                                                                                                                                                                                                                                                                    Streptococcus.
NCBI_TaxID=1314;
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ELKNOEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 VSIDGIQSLSFDIETINKKAVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90
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                                                                                                                                                  I -> L (in Ref. 2).
TNKGWYTAQELDYK -> QIKNGNCSRISYT (in Ref.
2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                             VT -> MK (in Ref. 2).
SQEVFAQQDPD -> LPKGICSTRPK (in Ref. 2).
H -> Q (in Ref. 2).
S -> N (in Ref. 2).
NLQNIYFLYEGDP -> TPKIYIFFMRVTL (in Ref.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29246 MW; 54001FE4CCCBFCC3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.2%; Score 1129; DB 1; 97.7%; Pred. No. 4.7e-65;
                                                               Exotoxin type A.
                                                                                    -> E (in Ref.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 4.76
1; Mismatches
Pfam; PF01123; Stap_Strp_toxin; 1.
PRINTS; PR00279; BACTRLTOXIN.
PROSITE; PS00277; STAPH STREP_TOXIN_1; 1.
PROSITE; PS00278; STAPH-STREP_TOXIN_2; 1.
3D-structure; Signal Toxin.
SIGNAL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 97.7
Matches 216, Conservative
                                                    30
251
128
6
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35
43
43
59
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117
17
25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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STRAND
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                                                               CHAIN
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Chaussee M.S.,

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91 ELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          outbreaks.;
Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
-!- FUNCTION: Causative agent of the symptoms associated with scarlet fever, have been associated with streptococcal toxic shock-like disease and may play a role in the early events of rheumatic fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There are no restrictions on ng as its content is in no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (By similarity).
SUBUNIT: Binds to major histocompatibility complex class II beta chain (By similarity).
SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
                                   Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin)
                                                                                                                                                                                                                                                                                                     PubMed=11917108; DOI=10.1073/pnas.062526099;
PubMed=11917108; DOI=10.1073/pnas.062526099;
Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S. Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Veasy L.G., Musser J.M., "Genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                       Streptococcus pyogenes (serotype M18). Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54001FE4CCCBFCC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFWFDFFPEPEFTQSKYLMIYKDNETLDSNT-QIEVYLTTK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 SFWFDFFFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.7e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Exotoxin type A. By similarity.
   25-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 1129; DB
; Pred. No. 4.7e-
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  By similarity
                                                                                             Name=speA; OrderedLocusNames=spyM18_0393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE009982; AAL97141.1; -.
InterPro; IPR008992; Bact endocox.
InterPro; IPR006177; Bctrl tox.
InterPro; IPR006123; Stap/Strep toxin.
InterPro; IPR006126; Stap/Strept tox.
InterPro; IPR006173; Staph.cx OB.
Pfam; PF02876; Stap Strp tox C; Pfam; PF02123; Stap_Strp_tox C; IPR06123; Stap_Strp_tox C; IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome; Signal; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 128 E
251 AA; 29246 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.2%;
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Matches 216; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00279; BACTR
                                                                                                                                                                                                                    NCBI_TaxID=186103;
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                           Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHDLIYNVSGPNYDKLKT 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
Hayashi H., Hattori M., Hamada S.;
"Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
"Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
large-scale genomic rearrangement in invasive strains and new insights
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                        MEDLINE=22133808; PubMed=12122206; DOI=10.1073/pnas.152298499; Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S., Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D. Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M., Schlievert P.M., Musser J.M.; Genome sequence of a serotype M3 strain of group A Streptococcus: phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
Streptococcus pyogenes (serotype M3).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 SFWFDFFPEPEFTQSKYLMIYKDNETLDSNT-QIEVYLTTK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 SFWFDFFPERFFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 AA; 29260 MW; 05E782CDA01BFCD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008192; Bact endotox.
InterPro; IPR006127; Bcrt tox.
InterPro; IPR006123; Stap/Strep toxin.
InterPro; IPR006126; Staph/Strept_tox.
InterPro; IPR006125; Staph/Strept_tox.
InterPro; IPR00613; Staph tox OB.
Pfam; PF01123; Stap Strp toxin; IPR0879; Stap Strp toxin; IPR0879; BACTRIOXIN; IPR0879; BACTRIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      into phage evolution.";
Genome Res. 13:1042-1155(2003).
EMBL; AR014161; AAM79908.1; -.
EMBL; AP005142; BAC63655.1; -.
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01-AUG-1988 (Rel. 08, Created)
01-JAN-1990 (Rel. 13, Last seq
                                                                                                                                                                                       Serotype M3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 98.2
Matches 217; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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HSSP; P01552; 1SEB.
                                                                                       NCBI_TaxID=198466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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SEQUENCE 251 AA
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Last sequence update)

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130 EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA 189
     294 ENFGYNQSVHQINRSDFSKQDWESQIDKELSQNQPVYYQGVGKVGGHAFVIDGADGRNFY 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AISTROYNWINILPTYSGRESNVOKMAISELMADVGISVDMDYGPSSGSAGSSRVQRALK 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENFGYNOSVHOINRSDFS-QDWEAQIDKELSQNQPVYYQG-GKVGCHAFVIDGADGRNFY 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENFGYNQSVHQINRSDFSKQDWEAQIDKELSQNQPVYYQGVGKVGGHAFVIDGADGRNFY 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 AISTROYNWINILPTYSGRESNVQKMAISELMADVGISVDMDYGPSSGSAGSSRVQRALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 FTQSKYLMIYKDNETLDSNTQIEVYLTT---KQPVVKSLLDSKGIHYNQGNPYNLLTPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=SP268;
MEDLINE=21655126; Pubmed=11796571; DOI=10.1128/IAI.70.2.462-469.2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jadoun J., Eyal O., Sela S.;
"Role of CarR, hyaluronic acid, and SpeB in the internalization of Streptococcus pyogenes M type 3 strain by epithelial cells.";
Infect. Immun. 70:462-469(2002).
EMBL, AX038886; AX71464.1; -.
GO, GO:0008234; F:cysteine-type peptidase activity; IEA.
GO, GO:0006808; P:proteclysis and peptidolysis; IEA.
InterPro; IPR000200; Peptidase C10.
PRINTS; PR00797; STREPOPAIN.
ProDom; PD004169; Peptidase_C10; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.7%; Score 1293.5; DB 2; Length 344; 91.3%; Pred. No. 1.7e-75; rive 5; Mismatches 8; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pyogenes.
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                              354 HVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        344 AA; 37345 MW; FB0A9BD05B541909 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Exotoxin type A-phage associated (SpeA precursor).
Name=speA3; OrderedLocusNames=SP80560, SpyM3_1301;
                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            461
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                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created 01-DEC-2001 (TrEMBLrel. 19, Last se 01-JUN-2003 (TrEMBLrel. 24, Last an Cysteine protease SpeB (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 91.3
Matches 251; Conservative
                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1314;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus
                                                                                                                                                                                                                                                                                         093L02;
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protease.
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NON TER
SEQUENCE
                                                              427
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                                                                                     DB 1; Length 398;
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STRAIN-NZ131;
Watanabe Y., Ohkuni H.;
Watanabe Y., Ohkuni H.;
Watanabe Y., Ohkuni H.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB051298; BAB40954.1; --
GO, GO.0008234; F.:Cysteine-type peptidase activity; IEA.
GO, GO.0005508; P.:proteolysis and peptidolysis; IEA.
InterPro; IPR000200; Peptidase C10.
Přam; PF01640; Peptidase C10; I.
PRINTS; PR00797; STREPTOPAIN.
PRODOM; PD004169; Peptidase C10; 1.
SEQUENCE 398 AA; 43218 MW; 07D1F534E7887CDD CRC64;
                                                                               53.1%; Score 1327.5; DB 1; Length ilarity 91.5%; Pred. No. 1.3e-77; Conservative 5; Mismatches 8; Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Last annotation update)
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EMBL; AE006625; AAK34706.1; -. EMBL; AE014170; AAM80349.1; -.
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01-JUN-2001 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
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Best Local Similarity
Matches 257; Conserv
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NCBI_TaxID=1314;
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MEDLINE=99081733; PubMed=9864206;
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   SEQUENCE FROM N.A.
SERAIN=SS1-1, Serotype M3;
STRAIN=SS1-1, Serotype M3;
MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
Hayashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
Hayashi H., Hattori M., Hamada S.,
"Genome sequence of an M3 train of Etreptococcus pyogenes reveals a
"Genome sequence of an M3 train of Etreptococcus pyogenes reveals a
large-scale genomic rearrangement in invasive strains and new insights
                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIM=SF310 / ATCC 700294 / Serotype M1;
MEDLINE=21192649; PubMed=11296296; DOI=1073/pnas.071559398;
MEDLINE=21192649; PubMed=11296296; DOI=1073/pnas.071559398;
Ferretti J.G., McShan W.M., Ajdic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.E.;
"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN+MGASB232 / Serotype M18;
PubMed=11917108; DOI=10.1073/pnas.062526099;
Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S., Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Farkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
"Genome sequence and comparative microairay analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=MGAS315 / Serotype M3;
MEDLINE=2133808; PubMed=12122206; DOI=10.1073/pnas.152298499;
MEDLINE=2133808; PubMed=12122206; DOI=10.1073/pnas.152298499;
MEDLINE=2133808; PubMed=12122206; DOI=10.1073/pnas.152298499;
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D., Campbell D.S., Smith T.W., McCormick J.K., Leung D.Y.M.,
"Genome sequence of a serotype M3 strain of group A Streptococcus:
"Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=76190087; PubMed=1270417; Blliott S.D.; Xortt A.A., Liu T.-Y., Blliott S.D.; In Yerimary structure of streptococcal proteinase. III. Isolation of cyanogen bromide peptides: complete covalent structure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY SEQUENCE OF 28-86 AND 121-398.
Yonaha K., Elliott S.D., Liu T.-Y.;
Primary structure of zymogen of streptococcal proteinase.";
J. Protein Chem. 1:317-334(1982).
                                                                     Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                               Hong K.;
"A novel cloning method used arbitrarily primed PCR.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide chain.";
J. Biol. Chem. 251:1955-1959(1976)
Microb. Pathog. 15:327-346(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=NZ131 / Serotype M49, T14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             into phage evolution.";
Genome Res. 13:1042-1055(2003)
                           SEQUENCE FROM N.A.
STRAIN=A-20 / Serotype M1,T1;
                                                                                                                 STRAIN=Sv / Serotype M23;
                                                                                              SEQUENCE FROM N.A.
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outbreaks.";
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FUNCTION.
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                                                                                                                                                          PUNCINE.

STRAIM-A-20 / Serotype MI, TI;

MEDLINE=99386817; PubMed=10456871;

TRai P.-J., Lin Y.-S., Kuo C.-F., Lei H.-Y., Wu J.-J.;

Trai P.-J., Lin Y.-S., Kuo C.-F., Lei H.-Y., Wu J.-J.;

Trai P.-J., Lin Y.-S., Kuo C.-F., Lei H.-Y., Wu J.-J.;

Trai D.-J., Lin Y.-S., Kuo C.-F., Lei H.-Y., Wu J.-J.;

Infect. Immun. 67:4334-4339(1999).

1-FUNCTION: Important streptococcal virulence factor which cleaves human fibronectin and degrades vitronectin. Also cleaves human LLIB precursor to form biologically active ILIB. Can induce apoptosis in human monocytes and epithelial cells in vitro, and reduces phagocytic activity in monocytic cells. Thus, may play a role in bacterial colonization, invasion, and inhibition of wound
                                        "Streptococcal pyrogenic exotoxin B induces apoptosis and reduces phagocytic activity in U937 cells."; Infect. Immun. 67:126-130(1999).
Kuo C.-F., Wu J.-J., Tsai P.-J., Kao F.-J., Lei H.-Y., Lin M.T.,
Lin Y.-S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- CATALYTIC ACTIVITY: Preferential cleavage with hydrophobic residues at P2, P1 and P1'.
-:- SUBCELLULAR LOCATION: Secreted.
-:- SIMILARITY: Belongs to the peptidase C10 family.
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AB030578; BAB16027.1; -
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L26430, AAA26997.1;
L26131, AAA26997.1;
L26132, AAA26998.1;
L26133, AAA26998.1;
L26134, AAA2700.1;
L26135, AAA2700.1;
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L26126; AAA26992.1;
L26127; AAA26993.1;
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AAA27014.1;
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L26162; AAA26991.1
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EMBL;
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Streptococcus.
NCBI_TaxID=1314, 198466, 186103;
                                                                                                                                           STANDARD;
19.5
19.5
19.3
19.2
                                       19.0
118.7
118.7
118.3
118.3
17.8
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                    482
479
478.5
475.5
468
                                                           468
457
454
445.5
444
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SPEB_STRPY
Q931q2 streptococc
Q8k6k5 streptococc
Q8779 streptococc
Q9779 streptococc
Q9745 streptococc
Q97453 streptococc
Q794Q streptococc
Q938p4 streptococc
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Q953A streptococc
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                                            September 17, 2005, 00:48:38; search time 148.406 Seconds (without alignments) 1614.846 Million cell updates/sec
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                                                                                     1 MQQDPDPSQLHRSSLVKNLQ.....ALGTGGGAGGFNGYQSAVVG 468
                                                                                                                                                                                                                                                                         Description
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005157
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Q68t49
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     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                      1612378 seqs, 512079187 residues
                                                                                                                                                                                                                                                    SUMMARIES
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ETC3 STAAM
006535
06ST49
ETC2 STAAU
ETC1 STAAU
                                                                                                                                                                                                                                                                                    SPEB STRPY
Q9AJD2
Q93LQ2
Q8K6K5
SPEA STRP8
SPEA STRPY
Q54779
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Q53678
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Maximum Match 1008
Listing first 45 summaries
                                OM protein - protein search, using sw model
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Q57453
Q79AQ0
Q54696
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Q8NXJ6
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Q9S5Z4
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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2500
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        487.5
        19.5
        260
        2
        079X14
        Q79X14 streptococc

        33
        487.5
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        2
        054739
        0764p6
        054739 streptococc

        34
        484
        19.4
        264
        2
        0764p6
        0764p6
        0764p6 staphylococ

        36
        478
        19.1
        259
        2
        0761s8
        0761s8 staphylococ

        37
        478.5
        19.1
        222
        2
        06XZE6
        06xze6 staphylococ

        38
        475.5
        19.0
        222
        2
        06XZE7
        06xze7 staphylococ

        40
        468
        18.7
        261
        2
        06xVM
        06ycm4 staphylococ

        41
        468
        18.7
        261
        2
        06FN0
        06gfn0 staphylococ

        41
        468
        18.7
        261
        2
        06XXM3
        06xxm3 staphylococ

        43
        457
        18.3
        261
        2
        06XXM4
        06xxm4 staphylococ

        44
        445.5
        17.8
        233
        2
        08RX77
        08rx77
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ALIGNMENTS

PRT, 198 AA, 1054064, 054065, 054065, 054065, 054066, 054065, 054066, 054065,

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enterotoxin D precursor - Staphylococcus aureus
CiSpecies: Staphylococcus aureus
CiSpecies: Staphylococcus aureus
CiSpecies: Staphylococcus aureus
CiAccession: A3393
RiBayles, K.W.; Iandolo, J.J.
J. Bacteriol. 171, 4799-4806, 1989
A.Title: Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin
A.Reference number: A33953; MUID:89359112; PMID:2549000
A.Reference number: A33953; MUID:89359112; PMID:2549000
A.Reference number: A38953
A.Residue: preliminary
A.Molecule type: DNA
A.Residues: 1-258 - KBMy>
A.Residues: 1-258 - KBMy>
A.Residues: 1-258 - KBMy>
A.Cocssiveries: UNIPROT:P20723; GB:M28521; NID:91492109; PIDN:AAB06195.1; PID:975869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TELKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSAC-IGGVTNREGNHLEIPKKIVV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 KVSIDGIQ-SLSFD-IETNKKKVTAQELDYKVRKYLTDNKQLYTNGP--SKYETGYIKFI 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 QLHR-----SSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYN---VSGPNYDKLK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :||: ||: ||: ||: || 36 ELHKKSELSSTALMNMKGRY--ADKNPIIGENKSTGDQPLENTLLYKKFFTDLINFEDLL 93
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 11.8%; Score 295.5; DB 2; Length 258; Best Local Similarity 35.0%; Pred. No. 5e-12; Matches 79; Conservative 44; Mismatches 86; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 PKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDS-NTQIEVYLTTK 220
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Search completed: September 17, 2005, 01:14:35 Job time : 35.847 secs



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A; Title: Revised sequence of the Porphyromonas gingivalis prtT cysteine protease/hemaggl A; Reference number: Z17199; MUID:95105001; PMID:7806362
A; Accession: T10890
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-886 cMbD>
A; Residues: 1-886 cMbD>
A; Crosser-references: UNIPROT:Q53481; EMBL:S75942; NID:g913136; PID:g913137
C; Generics:
A; Gene: prtT
C; Keywords: cysteine proteinase; hemagglutinin; hydrolase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 LEIP--KKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYE 168
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                                                                                                                                                                                                                             2 QODPDPSQLHRSSLVKN----LQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYD 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 FDNGNLQNVLIRVYENKRNTISFEVQTDKKSVTAQELDIKARNFLINKKNLYEFNSSPYE
                                                                                                                                                                                  2 QODPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSG---PNYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 TGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTVDSKSVKIEVHLTTK 264
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                                              Length 266;
                                                                                                              70; Indels
                                       ; Score 509; DB 1;
;; Pred. No. 7.5e-26;
44; Mismatches 70
                                          Query Match
Best Local Similarity 44.7%;
Matches 105; Conservative 4.
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17.8%;
Best Local Similarity 43.3%;
Matches 101; Conservative
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cysteine proteinase (EC 3.4.22.-) / hemagglutinin protein - Porphyromonas gingivalis C;Species: Porphyromonas gingivalis C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

R;Madden, T.E.; Clark, V.L.; Kuramitsu, H.K. Infect. Immun. 63, 238-247, 1995

Accession: T10890

RESULT 13

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A,Cross-references: UNIPROT:099T49; GB:BA000018; PID:g13701619; PIDN:BAB42912.1; GSPDB:C-A,Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cispecies: Stappylococcus aureus
Cipate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
Cipate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
Cipate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
Ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
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                                                                                                                                                                                                                                                                                                                                 408
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                                                                                                              289
                                                                                                                                                               224
                                                                                                                                                                                                                        349
                                                                                                                                                                                                                                                       225 DYYDDWTGTH-THYSGTFG----ETYNWSKMPGNISVGISPEEVKALSTFMRDVSFSVNM 279
                                                                                                                                                                                                                                                                                                                                                                   280 QFADFGSGTFSIFVERALRETFHYKKSLRYIHRSLLPGKEWKOMIRKELAENRPVYYAGA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                KVG-GHAFV1DGADGRNFYHVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVV 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         340 DGSMGHAFVCDGYEPDGTFHFNWGWGGMSNGNPYLNLLNPGSLGTGAGDGGYSTDQEVVI 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 VRNYLLKHKOL/YEFNSSPYETGYIKFIEGSGHSFWYDLMPESGKKFYPTKYLLIYNDNKT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 ERSACIGGVTNREGNHL-----EIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               XKTCMYGGVTEHDGNQIDKNNSTDNSHNILIKVYENERNSLSFDIPTNKKNITAQEIDYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPE--PEFTQSKYLMIYKDNET
                                                                                                                                           DYGPSSGSAGSSRVQRALKENFGYNQSVHQINRSDF-SQDWEAQIDKELSQNQPVYYQGG
                                                                                                                                                                                                                          TYTLSSNNPYFNHPKNLFAA1STRQYNWNN1LPTYSGRESNVQKMA1SELMADVG1SVDM
                                                                                                              230 SKGIHYNQGNPYNLLTPVIEKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                        16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enterotoxin YENT2 [imported] - Staphylococcus aureus (strain N315)
                                                        94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39;
Query Match
16.9%; Score 422; DB 2;
Best Local Similarity 39.0%; Pred. No. 1.8e-19;
Matches 94; Conservative 37; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.1%; Score 303.5; DB 47.4%; Pred. No. 6e-13; Partive 23; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDSNT-QIEVYLTTK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Best Local Similarity
Matches 64; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-136 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G 400
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A; Molecule type: protein
A; Residues: 28-66 cB0H2>
B; Couch, J.L.; Betley, M.J.
J. Bacteriol. 171, 4507-4510, 1989
A; Title: Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests t]
A; Accession: A33866; MUID:89327174; PMID:2473979
A; Accession: A33866
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-266 cCOU>
A; Cross-references: GB:M28364; NID:g153003; PIDN:AAA26624.1; PID:g153004
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A; Residues: 1-266 <BOH3
A; Cross-references: UNIPROT:P01553; EMBL:X05815; NID:g46566; PIDN:CAA29260.1; PID:g4656',
R; Schmidt, J.J.; Spero, L.
J. Biol. Chem. 258, 6300-6306, 1983
A; Title: The complete amino acid sequence of Staphylococcal enterotoxin C-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 LEIP--KKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYE 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 QPDPTPDELHKSSEFTGTMGNMKYLYDDHYVSATKVMSVDKFLAHDLIYNISDKKLKNYD 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Staphylococcus aureus
C;Date: 15-Nov-1984 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
C;Date: 15-Nov-1984 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
C;Accession: 806356; A01816
R;Bohach, G.A.; Schlievert, P.M.
Mol. Gen. Genet. 209, 15-20, 1987
A;Title: Nucleotide sequence of the staphylococcal enterotoxin C1 gene and A;Reference number: 806356; MUID:88038352; PMID:2823067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |-|||| | |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |---| |--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 FDNGNLQNVLIRVYENKRNTISFEVQTDKKSVTAQELDIKARNFLINKKNLYEFNSSPYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 KLKTELKNQEMATLFKDKNIDIYGVEYYHLCYLCE-----NAERSACIGGVTNREGNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 QODPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSG---PNYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 TGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNETLDS-NTQIEVYLTTK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 TGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTVDSKSVKIEVHLTTK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
20.4%; Score 510; DB 2; Length 266;
Best Local Similarity 44.3%; Pred. No. 6.4e-26;
Matches 104; Conservative 45; Mismatches 70; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Superfamily: enterotoxin B
;Seywords: enterotoxin
;1-27/Domain: signal sequence #status predicted <SIG>
;28-266/Product: enterotoxin C-1 #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Gene: entC2
C,Superfamily: enterotoxin B
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-266/Product: enterotoxin C-2 #status predicted <MAT>
                A; Reference number: A60114; MUID: 89277549; PMID: 2543637
                                                        A;Accession: A60114
A;Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 28-75,'IL',78-176,'N',178-266 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;28-266/Product: enterotoxin C-1 #status exper:
F;120-137/Disulfide bonds: #status experimental
                                                                                                                                                                    A;Residues: 1-266 <BOH>
A;Cross-references: UNIPROT:P34071
A;Accession: B60114
                                                                                                                                    A;Molecule type: DNA
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Milternate names: enterotoxin C-3 precursor

C;Species Staphylococcus aureus

C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004

C;Accession: A60114; B60144; A31866

R;Bohach, G.A.; Schlievert, P.M.

Infect. Immun. 57, 2249-2255, 1999

A;Title: Conservation of the biologically active portions of staphylococcal enterotoxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Accession: S11885
R.Hovde., C.J.; Hackett, S.P.; Bohach, G.A.
Mol. Gen. Genet. 220, 329-333, 1990
A;Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence comparity A;Accession: S11885; MUD: 90220508; PMID: 2325627
A;Accession: S11885
A;Accession: S11885
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-266 <HOV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P23313; GB:X51661; NID:g46570; PIDN:CAA35972.1; PID:g46571 C;Superfamily: enterotoxin B
                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 KLKTELKNQEMATLFKDKNIDIYGVEYYHLCYLCENA------ERSACI-GGVTNRE 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKY 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLKTELKNOEMATLFKDKNIDIYGVEYYHLCYLCE-----NAERSACIGGVTNREGNH 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 KVKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNVGKVTGGKTCMYGGITKHEGNH 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEIP--KKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYE 168
                                                                                                                                                                                                                                                                                                                                                                 QODPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSG---PNYD 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||||||| :|| :|||||| | :|||||||||| | ETGYIKFI-ENENSFWYDMPAPGDKEDGSKYLMMYDGKDVKIEVYLTTKK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Staphylococcus aureus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNETLDS-NTQIEVYLTTKQ 221
                                                                                                                                                                                                                                                                                                                 2 QODPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGP---NYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 TGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTVDSKSVKIEVHLTTK 264
                                                                                                                                                                                                                                                 18;
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                                                                                                                                                                Length 266;
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                                                                                                                                                                                                                                             67; Indels
    F;1-27/Domain: signal sequence #status predicted <SIG>F;28-266/Product: enterotoxin B #status experimental <MAT>F;120-140/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.5%; Score 513; DB 2; L. 45.1%; Pred. No. 4.1e-26; Live 43; Mismatches 70;
                                                                                                                                                            21.6%; Score 541; DB 1; 47.7%; Pred. No. 6.3e-28; ative 39; Mismatches 67;
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Matches 106; Conservative
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                        Query Match
Best Local Similarity
F;1-27/Domain: signal
                                                                                                                                                                                                                                 Matches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168
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16;

110 149 209

gene and relatedness

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A;Residues: 28-42;128-148 <ALA>
C;Superfamily: enterotoxin B
C;Keywords: enterotoxin; extracellular protein; toxin
A;Residues: 1-250 <JOH>
A;Cross-references: UNIPROT:P08095
C;Superfamily: enterotoxin B
C;Keywords: exotoxin
                                                                                                                                                                Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184
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C;Species: Streptococcus pyogenes
C;Species: Streptococcus pyogenes
A;Variety: Strain MGAS262 isolate California
C;Date: 29-Jan-1993 #text_change 09-Jul-2004
C;Accession: S18789
R;Nelson, K; Schlievert, P.M; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A;Title: Characterization and clonal distribution of four alleles of the speA gene encod A;Reference number: S18782; MUID:92044323; PMID:1940804
A;Accession: S18789
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 cMEL.
A;Cross-references: UNIPROT:Q54696; EMBL:X61573; NID:g47303; PIDN:CAA43771.1; PID:g47304
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: enterotoxin B
C;Keywords: exotoxin
F;1-22/Domain: signal sequence (fragment) #status predicted cSIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sta
                                                                                                                                                                                                                                                                                                                                                                                     exotoxin A precursor (allele 4) - Streptococcus pyogenes (strain MGAS262 isolate Califor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C,Accession: A26152
R;Johnson, D.P.; L'Italien, J.J.; Schlievert, P.M.
Mol. Gen. Genet. 203, 354-356, 1986
A;Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to A,Reference number: A26152; MUID:86284313; PMID:3526093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ï
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                                                    83 ELKNQEMATLFKDKNVDIYSVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 142
                                                                                                                                         ELKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QODPPPSQLHRSSLVKNLQNIYFLYEGDPVVHENVKSVDQLLSHDLIYNVSGLNYDKLKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.5%; Score 986.5; DB 2
88.2%; Pred. No. 6.9e-57;
iive 13; Mismatches 11
                                                                                                                                                                                                                                        203 SFWFDFFPEPEFTOSKYLMIYKDNETLDSNT 233
                                                                                                                                                                                                             181 SFWFDFFPEFFTQSKYLMIYKDNETLDSNT 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 SFWFDFFPEPEFTQSKYLMIYKDNETLDSNT 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 88.23
Matches 186; Conservative
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A;Molecule type: DNA
A;Residues: 1-266 <JON>
A;Cross-references: UNIPROT:P01552; EMBL:M11118; NID:g152999; PIDN:AAA88550.1; PID:g1530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rithung, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3518-3525, 1970
J. Reference number: A92065; MUID:71007902; PMID:5470821
J. Residues: 28-55, NND', 59-68, NE', 71, 'FDLIYL', 78-117,119-127, 'N',129,'D', 131-132,'ENT', J. Experimental source: strain S-6
R. Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3511-3517, 1970
J. Biol. Chem. 245, 3511-3517, 1970
J. Holl. The primary structure of staphylococcal enterotoxin B. II. Isolation, composit: A;Reference number: A92064; MUID:71007901; PMID:5470820
J. Reference number: chymotryptic peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rithang I.Y.; Bergdoll, M.S.

Rithang I.Y.; Bergdoll, M.S.

Biol. Chem. 245, 3493-3510, 1970

A;Title: The primary structure of staphylococcal enterotoxin B. I. Isolation, compositic A;Reference number: A92063; MUID:71007900; PMID:5470819

A;Contents: annotation; tryptic peptides

A;Contents: annotation; tryptic peptides

Rischantz, E.J.; Reseslar, W.G.; Wagman, J.; Spero, L.; Dunnery, D.A.; Bergdoll, M.S.

Biochemistry 4, 1011-1016, 1965

A;Title: Purification of staphylococcal enterotoxin B.

A;Title: Purification of staphylococcal enterotoxin B.

A;Title: Johnsky, E.Y.; Kolosov, M.I.; Maurer-Fogy, I.; Moskaleva, E.Y.; Sveshni R;Alakhov, V.Y.; Klinsky, E.Y.; Kolosov, M.I.; Maurer-Fogy, I.; Moskaleva, E.Y.; Sveshni A;Title: Identification of functionally active fragments of staphylococcal enterotoxin B.

A;Title: Identification of functionally active fragments of staphylococcal enterotoxin B.

A;Reference number: S27240; MUID:93049338; PMID:1425690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enterotoxin B precursor - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 24-Apr-1994 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C;Accession: S27360; A92065; S27240; A01815
R;Jones, C.L.; Khan, S.A.
J. Bacteriol. 166, 29-33, 1986
A;Title: Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.
A;Reference number: S27360; MUID:86168029; PMID:3957869
                                                                                                                                                                                                                                                                                                                                         NQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVKVSI 123
                                                                                                                                                                                                                                                                                                                                                                                     94 NQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACLYGGVTNHEGNHLEIPKKIVVKVSI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFW 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93
                                                                                                                                                                                                                           5 PDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKTELK
                                                                               Gaps
                                                                               ë,
                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FDFFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FDFFPEPEFTQSKYLMIYKDNETLDSNT-QIEVYLTTK 220
                                                                                   25;
Score 938.5; DB 1
Pred. No. 9.8e-54;
5; Mismatches 25
37.5%;
84.9%;
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11:55:40 2005

17

Sep

Sat

strain

enco

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A; Status: nucleic acid sequence not snown; translation not snown
A; Residues: 1-236 < NEA>
A; Cross-references: EMEL:X61562; NID:947299; PIDN:CAA43760.1; PID:947300
A; Experimental source: strain MGAS251 isolate California unassignd phage
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A; Accession: S18788
A; Accession: S18788
A; Residues: 1-236 < NEZ>
A; Cross-references: EMBL:X61563; NID:947301; PIDN:CAA43761.1; PID:947302
A; Residues: 1-236 < NEZ>
A; Cross-references: EMBL:X61563; NID:947301; PIDN:CAA43761.1; PID:947302
A; Residues: 1-236 < NEZ>
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A; Accession: S18790
A; Residues: 1-236 < NEZ>
A; Residues: 1-
                                                                         Cispecies: Streptococcus pyogenes phage
A;Variety: strain MGAS250 isolate California; strain MGAS251 isolate California; strain phage
B;Variety: strain MGAS250 isolate California; strain MGAS251 isolate California; strain phages
B;Variety: strain MGAS250 isolate Garmany
C;Date: 29-3na-1993 #sequence revision 29-3na-1993 #text change 16-Jul-1999
C;Accession: S18786; S18787; S18788; S18790; S18792; S18795; S18799
C;Accession: S18786; S18787; S2 S18790; S18792; S18795; S18799
J. Exp. Med. 174, 1271-1274, 1991
A;Title: Characterization and clonal distribution of four alleles of the speA gene encony, A;Reference number: S18782; MUID:92044323; PMID:1940804
A;Reference number: S18786
A;Reference number: S18786
A;Residues: 1-236 <ABL>
A;Residues: 1-236 <ABL>
A;Cross-references: EMEL>
A;Cross-references: Emelain MGAS250 isolate California unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
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A;Residues: 1-236 <NEO>
A;Cross-references: EMBL.X61565; NID:g47311; PIDN:CAA43763.1; PID:g47312
A;Cross-references: Extain MGAS480 isolate Yugoslavia unassigned phage
A;Rote: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: S18787
A;Status: nucleic acid sequence not shown; translation not shown
                                              N; Alternate names: scarlet fever toxin
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A; Residues: 1-236 <a href="https://www.nciercons.com
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A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-236 cMED>
A; Cross-references: EMBL:X61571; NID:947323; PIDN:CAA43769.1; PID:947324
A; Experimental source: strain MGAS495 isolate Germany unassigned phage
A; Cross-references: sequence was submitted to the EMBL Data Library, September 1991
C; Genetics:
A; Genetics: A; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; G
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A;Experimental source: strain MGAS491 isolate United Kingdom unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18801
A;Accession: signal acid sequence not shown; translation not shown
A;Molecule type: DNA
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A;Experimental source: strain MGAS624 isolate Germany unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A,Variety: strain MGASIS8 isolate Nebraska; strain MGAS485 isolate Yugoslavia; strain C;Date: 29-Jan-1993 #sequence revision 29-Jan-1993 #text_change 16-Jul-1999 C;Accession: S18793; S18794; S18801; S18798 R;Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
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                                                                                                                                                                                                                                                                                                                                 A, Title: Characterization and clonal distribution of four alleles
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A, Status: nucleic acid sequence not shown; translation not shown
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Best Local Similarity 98.6
Matches 208; Conservative
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A;Residues: 1-216 <NEH>
A;Cross-references: EMBL:X61566; NID:g47317; PIDN:CAA43764.1; PID:g47318
A;Experimental source: strain MGAS492 isolate United Kingdom unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X61567; NID:947325; PIDN:CAA43765.1; PID:947326
A;Experimental source: strain MGAS496 isolate Germany unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QODPDPSQLHRSSLVKNLQNI YFLYBGDPVTHENVKSVDQLLSHDLI YNVSGPNYDKLKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Ke^words: exotoxin
F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F;23-236/Product: exotoxin type A (fragment) #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 236;
A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                            A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1089.5; DB 2; Length
Pred. No. 1.5e-63;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 97.6°
Matches 206; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Superfamily: enterotoxin B
                                                                                                                                                                                                                                                                                                                    A; Residues: 1-236 <NES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
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- Streptococcus pyogenes phage (strain MGAS250 isol

exotoxin type A precursor (allele 2)

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A; Experimental source: Streptococcus pyogenes strain MGAS165 isolate Minnesota unassigne Aylote: the nucleotide sequence was submitted to the EMBL Data Library, September 1991 A;Accession: S18785 A;Status: nucleic acid sequence not shown; translation not shown
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A;Experimental source: Streptococcus pyogenes strain MGAS500 isolate New Zealand unassiy
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exotoxin type A precursor (allele 3) - Streptococcus pyogenes phage (strain MGAS158 isol
N;Alternate names: scarlet fever toxin
C;Species: Streptococcus pyogenes phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X61555; NID:947309; PIDN:CAA43753.1; PID:947310
A;Experimental source: Streptococcus pyogenes strain MGAS327 isolate Arizona unassigned
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 9-244 <NBO.
A; Cross-references: EMBL:X61557; NID:g47319; PIDN:CAA43755.1; PID:g47320
A; Experimental source: Streptococcus pyogenes strain MGAS493 isolate France unassigned
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 9-244 «NEH»
A; Cross-references: EMBL:X61558; NID:947321; PIDN:CAA43756.1; PID:947322
A; Experimental source: Streptococcus pyogenes strain MGAS494 isolate France unassigned
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
                                                                                                                                                                                                                                                                                   A,Molecule type: DNA
A,Residues: 9-244 (MEZ>
A,Cross-references: EMBL.X61559, NID:947293; PIDN:CAA43757.1; PID:947294
A,Experimental source: Streptococcus pyogenes strain MGAS167 isolate Texas unassigned I
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 ELKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 VSIDGIQSLSFDIETNKRAVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QODPDPSQLHRSSLVKNLQNI YFLYEGDPVTHENVKSVDQLLSHDLI YNVSGPNYDKLKT
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                                           A;Residues: 9-244 <NEA>
A;Cross-references: EMBL:X61556; NID:g47291; PIDN:CAA43754.1; PID:g47292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: S18796
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: S18797
A;Status: nucleic acid sequence not shown; translation not shown
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A;Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFWFDFFPBFBFTQSKYLMIYKONETLDSNTSQIEVYLTTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1129; DB 1;
Pred. No. 4.4e-66;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 97.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 9-228 <NES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 9-244 <NEY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S18791
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N.Alternate names: erythrogenic toxin; scarlet fever toxin
Cispecies: Streptococcus pyogenes phage T12
Cibate: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 10-Sep-1999
CiAccession: S29659; S18782; S18784; S18785; S18791; S18796; S18797; S18800
Riwecks, C.K.; Ferretti, J.J.
Infect: Immun: 52, 144-150, 1986
A;Title: Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) g
A;Accession: S29659; MUID:86166804; PMID:3514452
A;Accession: S29659; MUID:86166804; PMID:3514452
A;Accession: S29659; MUID:86166804; PMID:3514452
A;Accession: S29659; MUID:86166804; PMID:3514452
A;Accession: S29659; MUID:92044323; NID:91940804
A;Accession: K.; Schlevert, P.M.; Selander, R.K.; Musser, J.M.
J. Title: Characterization and clonal distribution of four alleles of the speA gene encod
A;Accession: S18782; MUID:92044323; PMID:1940804
A;Accession: S18782
A;Accession: S18782
A;Accession: S18782
A;Accession: S18784
A;Residues: 9-244 <a href="https://docession.com/massigned/A;Accession: S18784">https://docession.com/massigned/A;Accession: S18784
A;Accession: S18784
A;Accession: S18784
A;Status: nucleic acid sequence not shown; translation not shown
A;Accession: S18784
A;Accession: S18784
A;Accession: S18784
A;Accession: S18784
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                            III. Isolation of cyanogen browi
                                                                                                             A; Molecule type: protein
A; Residues: 1-337 < YON.
A; Residues: 1-337 < YON.
Title: View of the work 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197 YLMIYKDNETLDSNTQIEVYLTT---KQPVVKSLLDSKGIHYNQGNPYNLLTPVIEKVKP 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 YVEQIKENKKLDT-----TYAGTAEIKQPVVKSLLDSKGIHYNQGNPYNLITPVIEKVKP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238 NQSVHQIDRGDFSKQDWEAQIDKELSQNQPVYYEGVGKVGGHAFVIDDGAGRNFYHVDWG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 GEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFAAISTR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 GEÓSFVGÓAÁTGHCVÁTATAQIMKÝHNÝPDKGLKNÝTÝTLSSNPDÝFDHPKNLFAAISTR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 QYNWNNILPTYSGRESNVQKWAISELMADVGISVDMDYGPSSGSAGSSRVQRALKENFGY 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      374 NOSVHQINRSDFS-QDWEAQIDKELSQNQPVYYQG-GKVGGHAFVIDGADGRNFYHVNWG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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    zymogen of streptococcal proteinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 47.9%; Score 1198; DB 1; Best Local Similarity 84.1%; Pred. No. 2.2e-70; Matches 233; Conservative 14; Mismatches 20;
    귱
A,Title: Primary structure
A,Reference number: S07668
A,Accession: S07668
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

September 17, 2005, 01:00:14; Search time 33.847 Seconds (without alignments) 1330.382 Million cell updates/sec ö

US-10-002-784A-27

2500 1 MQQDPDFSQLHRSSLVKNLQ......ALGTGGGAGGFNGYQSAVVG 468 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

exotoxin type A prexotoxin type A prexotoxin type A prexotoxin type A prexotoxin A precurs streptococcal pyroenterotoxin B precentations enterotoxin (3 - S enterotoxin (-2 pr enterotoxin (-1 pr extracellular ente enterotoxin YENT2 enterotoxin Dorec enterotoxin SeO [i enterotoxin P [imp extracellular ente enterotoxin SeN [i enterotoxin A prec enterotoxin E prec enterotoxin SEM [i extracellular ente enterotoxin Yentl hypothetical prote hypothetical prote streptococcal pyro streptopain (EC 3. cysteine proteinas exotoxin 11 [impor probable flagellin exotoxin C precurs Description SUMMARIES BPSOP S29659 S18783 S18786 S18789 A26152 S11885 A60114 ENSAC1 A33953 E89969 G89991 H89968 A28664 A28179 D89969 C89969 B89969 G71609 D89807 G81361 G89968 r10890 489969 289984 Query Match Length DB 136 258 258 250 250 257 257 257 257 257 1327.5 1129 1096.5 1089.5 986.5 938.5 303.5 295.5 201.5 201.5 201.5 201.5 202.5 Score Result Š.

conserved hypothet	hypothetical prote	exotoxin 15 [impor	cytotoxin-associat	DNA-directed RNA p	conserved hypothet	zinc metalloprotei	hypothetical prote	rhoptry protein -	hypothetical prote	ORF MSV152 probabl	penicillin-binding	cag pathogenicity	desmocollin 1b pre	desmocollin la pre	Dscla precursor -
F90559	G82885	C89808	B48281	S72284	A89922	H95076	AD1541	T28676	D89991	T28313	S16624	C64588	B48910	A48910	137281
~	7	N	~	N	N	7	N	7	~	~	~	7	~	~	7
1183	616	227	1215	096	1146	1881	378	2401	351	1306	675	1186	770	824	840
5.0	4.9	4.9	4.9	4.9	4.9	4.8	4.8	4.8	4.8	4.7	4.7	4.7	4.7	4.7	4.7
124.5	123.5	123	123	122.5	122.5	121	120.5	120.5	119	118	117	117	116.5	116.5	116.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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gene and Gispecies: Streptococcal pyrogenic exotoxin type B precursor - Streptococcus pyogenes Cispecies: Streptococcus pyogenes Cispecies: Streptococcus pyogenes Cispecies: Streptococcus pyogenes Cistes 31-May-1991 #sequence_revision 31-May-1991 #text_change 22-Jun-1999 Cistes and Animater, A.R.; Schilevert, P.M.
J. Bacteriol. 172, 4536-4427, 1990
A;Title: Nucleotide sequence of the streptococcal pyrogenic exotoxin type B A;Reference number: A37768; MUID:90330563; PMID:2198264
A;Status: preliminary
A;Sobcule type: DNA

e E

A;Residues: 1-398 <HAU> A;Cross-references: GB:M86905; GB:M35110; NID:g153818; PIDN:AAA26978.1; PID:g153819 C;Superfamily: streptococcal cysteine proteinase C; Keywords: exotoxin

Gaps 11; DB 2; Length 398; Query Match 53.1%; Score 1327.5; DB 2; Length Best Local Similarity 91.5%; Pred. No. 1.1e-78; Matches 258; Conservative 5; Mismatches 8; Indels

5

192 FTQSKYLMIYKDNETLDSNTQIEVYLTT----KQPVVKSLLDSKGIHYNQGNPYNLLTPVI 120 ઠે d

EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA 308 AISTROYNWNNILPTYSGRESNVOKMAISELMADVGISVDMDYGPSSGSAGSSRVORALK 368 174 309 g δ

249

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234 요

ENFGYNOSVHOINRSDFS-QDWEAQIDKELSQNQPVYYQG-GKVGGHAFVIDGADGRNFY 426 ENFGYNQSVHQINRSDFSKQDWEAQIDKELSQNQPVYYQGVGKVGGHAFVIDGADGRNFY 353 369 294 ò 셤

à 셤

RESULT 2

streptopain (BC 3.4.22.10) precursor - Streptococcus pyogenes

N.Alternate names: streptococcal cysteine proteinase; streptococcal peptidase A
C;Species: Streptococcus pyogenes
C;Date: 24-Apr-1984 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
C;Accession: 807668; A00978
R;Yonaha, K.; B116tt, S.D.; Liu, T.Y.
J. Protein Chem. 1, 317-334, 1982

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 ELKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
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44.9%; Score 1122; DB 9; Length 251;
Best Local Similarity 97.3%; Pred. No. 1.2e-75;
Matches 215; Conservative 1; Mismatches 3; Indels
RESUL: 1.5
US-09-138-830-13
i Sequence 13, Application US/09308830
; Publication No. US20020086813A1
; GENERAL INPORMATION:
; APPLICANT: Regents of the University of Minnesota
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A
TITLE OF INVENTION: AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFWFDFFPEPEFTQSKYLMIYKONETLDSNTSQIEVYLTTK 251
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                                                                                                                                                         NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:
ADDRESSERE: Merchant & Gould P.C.
STREET: P.O. Box 2903
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402-0903
COMPUTER: MN
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
CORPUTER: IBM Compatible
COMPUTER: IBM Compatible
CORPUTER: IBM Compatible
COPERATING SYSTEM: DOS
SOFTWARE: PRESENG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/308,830
FILING DATE: 04-Aug-11999
CLASSIFICATION NUMBER: ECT/US97/2228
FILING DATE: 05-DEC-1997
APPLICATION NUMBER: 60/032,930
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAMME: SKOOG, MARK T
REGISTRATION NUMBER: 40,178
REFERENCE/DOCKET NUMBER: 600.346USWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-308-830-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
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Search completed: September 17, 2005, 01:05:40 Job time : 146.152 secs



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91 ELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
                                                                                                                                                                                                                                                                                                                                                                           91 ELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
                                                                                                                                                                                                                                                                              31 QQDPDFSQLHRSSLVKNLQNIXFLXEGDPVTHENVKSVDQLLSHDLIYNVSGPNYDKLKT 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/08973391A
; Sequence 13, Application US/08973391A
; Publication No. USZ0020054887A1
; Fublication No. USZ0020054887A1
; GREERAL INFORMATION:
APPLICANT: Schlievert, Patrick M.
APPLICANT: Schlievert, Patrick M.
APPLICANT: Stocht, Manuela
APPLICANT: Stocht, Jennifer
; APPLICANT: Oblendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF U
FILE REFERENCE: 600.3111WG OF STREPTOCOCCAL TOXIN A AND METHODS OF U
FILE REFERENCE: 600.3111WG OF STREPTOCOCCAL TOXIN A AND METHODS OF U
FILE REPERENCE: 1998-03-12
; FRIOR APPLICATION NUMBER: US/08/973,391A
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR PLILNG DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 251;
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                                                                                                                                                                                                Indels
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                                                                                                                                         Query Match 45.2%; Score 1129; DB 16; Best Local Similarity 97.7%; Pred. No. 3.7e-76; Matches 216; Conservative 1; Mismatches 2;
                    LENGTH: 251
TYPE: PRT
ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Streptococcus pyogenes
                                                                                             US-10-428-817A-163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-973-391A-13
SEQ ID NO 163
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JAPPLICANT: TERMAN, David S

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 38473-189118

CURRENT APPLICATION NUMBER: US/10/428,817A

CURRENT FILING DATE: 2003-05-05

PRIOR APPLICATION NUMBER: US 60/378,988

PRIOR APPLICATION NUMBER: US 60/389,366

PRIOR APPLICATION NUMBER: US 60/406,697

PRIOR PILING DATE: 2002-06-15

PRIOR APPLICATION NUMBER: US 60/406,750

PRIOR PILING DATE: 2002-06-09

PRIOR PILING DATE: 2002-06-01

PRIOR PILING DATE: 2002-06-01

PRIOR PILING DATE: 2002-10-01

PRIOR FILING DATE: 2002-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 ELKNQEMATLFKDKAVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 VSIDGIQSLSFDIETNKKAVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKT 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 251;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.4%; Score 1136; DB 17; 98.2%; Pred. No. 1.1e-76;
                                                                                                                                                              ATTORNEY ON TOWNER: US/08/882,431B
FILING DATE: Unne 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <UNANOMINICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-7014
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                  SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/767,687
FILING DATE: 29-Jan-2004
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
OPERATING SYSTEM: Macintosh 7.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
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PRIOR FILING DATE: 2003-01-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S-10-428-817A-163
Sequence 163, Application US/10428817A
Publication No. US20040214783A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NOS: 224
PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 98.29
Matches 217; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-767-687-16
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181 SFWFDFFPEPEFTQSKYLMIYKDNETLDSNT-QIEVYLTTK 220
                                                                                               211 SFWFDFFPEPEFTQSKYLMIYKONETLDSNTSQIEVYLTTK 251
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                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOCTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 16
LENGTH: 251
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                                                                                                                                                                                                                                                          ; Sequence 16, Application US/10002784A; Publication No. US20030036644A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Apple Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16, Application US/10767687
Publication No. US20050064526A1
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 98.2%
Matches 217, Conservative
                                                                                                                                                                                                           RESULT 11
US-10-002-7,84A-16
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US-10-767-687-16
        151
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Sequence 16, Application US/0882431

GENERAL INPORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 16
CORRESPONDENCE S: 16
CORRESPONDENCE JOHN Moran
STREET: US Army MRMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
COUNTRY: OSA
STATE: MARYLAND
COUNTRY: USA
COMPUTER READBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
COMPUTER: Macrosoft Word 6.0
CURRENT APPLICATION DATA:
MEDIUM TAND DATA:
MEDIUM TA
                                TELKNOEMATLFKDKNIDIYGVEYYHLCYLCENAERSACIGGVTNREGNHLEIPKKIVVK 120
                                                                                                                    180
                                                                                                                                                  VSIDGIQSLSFDIETNKKAVTTAQELDYKVTKYTTDNKQLYTNGPSKYETGYIKFIPKNKE 180
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TELKNOEMATLFKDKNIDIYGVEYYHLCYLCENAERSACIGGVTNREGNHLEIPKKIVVK
                                                                                                                 VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE
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                                                                                                                                                                                                                                                                SFWFDFFPEPEFTQSKYLMIYKONETLDSNTQIEVYLTTK 220
                                                                                                                                                                                                                                SFWFDFFPEPEFTQSKYLMIYKDNETLDSNTQIEVYLITK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MOTAIN, JOHN
REGISTRATION NUMBER:
TELEPHONE: (301) 619-2065
TELEPHONE: (301) 619-714
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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Matches 217; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Charles H. Harris
ADDRESSE: Charles H. Harris
STREBT: US Army MRMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent ACITY: FORT DETRICK
STATE: MARYLAND
62 ELKNOEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 VSIDGIQSLSFDIETNKKAVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *QQDPDPSQLHRSSLVKNLQN1YFLYEGDPVTHENVKSVDQLRSHDL1YNVSGPNYDKLKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: streptococcal pyrogenic exotoxin-A mutant
US-10-002-784A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFWFDFFPEPEFTQSKYLMIYKDNETLDSNT-QIEVYLTTK 220
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US-10-002-784A-26
                                                                                                                                                                                                                                               LENGTH: 371
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                                                                                                                                                                                                                                                                     TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 ENFGYNQSVHQINRGDFSKQDWEAQIDKELSQNQPVYYQGVGKVGGHAFVIDGADGRNFY 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENFGYNGSVHQINRSDFS-QDWEAQIDKELSQNQPVYYQG-GKVGGHAFVIDGADGRNFY 426
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US-11-021-951-25

Sequence 25, Application US/11021951

Publication No. US20050175581A1

GENERAL INPORMATION:
APPLICANT: HAUPTS, Ulrich
APPLICANT: KOLTERMANN, Andre
APPLICANT: SCHEIDIG, Andreas
APPLICANT: COCO, Wayne Michael
TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
TITLE OF INVENTION: Number: US/11/021,951
CURRENT APPLICATION NUMBER: US/21/021,951
CURRENT FILING DATE: 2004-12-22
PRIOR FILING DATE: 2004-06-18
PRIOR FILING DATE: 2004-06-18

PRIOR FILING DATE: 2004-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Gaps
        Sequence 25, Application US/10872197A

| Sequence 25, Application US/10872197A
| Publication No. US20050059126A1
| GENERAL INFORMATION:
| APPLICANT: Ulrich Hauprs
| APPLICANT: Andreas SCHEIDIG
| APPLICANT: Andreas SCHEIDIG
| APPLICANT: Ulrich KETTLING
| PRIME REPRENCE: 04156.0002U3
| CURRENT APPLICATION NUMBER: US/10/872,197A
| CURRENT FILING DATE: 2003-11-25
| PRIOR APPLICATION NUMBER: EP 03025871
| PRIOR APPLICATION NUMBER: EP 03025871
| PRIOR APPLICATION NUMBER: EP 03013819
| PRIOR PILING DATE: 2003-11-10
| PRIOR FILING DATE: 2003-11-10
| PRIOR FILING DATE: 2003-11-10
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1316.5; DB 17; Lengt
Pred. No. 6e-90;
4; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 52.7%;
Best Local Similarity 91.1%;
Matches 257; Conservative
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US-10-872-197A-25
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EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192 FTQSKYLMIYKDNETLDSNTQIEVYLTT----KQPVVKSLLDSKGIHYNQGNPYNLLTPVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 20; Length 371;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR PRILIGE DATE: 90-01-31; 09/144,776
PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 26
LENGTH: 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 46.7%; Score 1168; DB 14; Best Local Similarity 100.0%; Pred. No. 3.7e-79; Matches 220; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.7%; Score 1316.5; Di
91.1%; Pred. No. 6e-90;
cive 4; Mismatches 1
PRIOR APPLICATION NUMBER: 60/524,960
PRIOR FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: EP 04003058
PRIOR FILING DATE: 2004-02-11
PRIOR FILING DATE: 2004-02-11
PRIOR FILING DATE: 2003-11-11
PRIOR FILING DATE: 2003-11-10
PRIOR FILING DATE: 2003-11-10
PRIOR FILING DATE: 2003-11-10
PRIOR FILING DATE: 2003-11-10
PRIOR FILING DATE: 2003-10-18
NUMBER OF SEQ ID NOS: 191
SOFTWARE: Patentin Version 3.1
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 26, Application US/10002784A; Publication No. US20030036644A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial sequence
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Matches 257; Conservative
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294 ENFGYNQSVHQINRGDFSKQDWEAQIDKELSQNQPVYYQGVGKVGGHAFVIDGADGRNFY 353
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                                                                         ENFGYNQSVHQINRSDFS-QDWEAQIDKELSQNQPVYYQG-GKVGGHAFVIDGADGRNFY
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Sequence 25, Application US/10872198

Publication No. US2005002897A1

GENERAL INFORMATION:

APPLICANT: Ulrich HAUPTS

APPLICANT: Andreas SCHEIDIG

APPLICANT: Andreas SCHEIDIG

APPLICANT: Christian VOETSMEIER

APPLICANT: Ulrich Kettling

TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF

FILE REFERENCE: 04156.000204

CURRENT PILING DATE: 2004-06-18

PRIOR APPLICATION NUMBER: 60/544,960

PRIOR APPLICATION NUMBER: 60/524,960

PRIOR APPLICATION NUMBER: EP 04003058

PRIOR APPLICATION NUMBER: EP 03025871

PRIOR APPLICATION NUMBER: EP 03025871

PRIOR APPLICATION NUMBER: EP 03025811

PRIOR PILING DATE: 2003-11-11

PRIOR PILING DATE: 2003-11-10

PRIOR FILING DATE: 2003-11-10

PRIOR PILING DATE: 2003-11-10
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Best Local Similarity 91.1%; Pred. No. 6e-90;
Matches 257; Conservative 4; Mismatches 10;
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US-10-872-198-25
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                                                                                                                                                                                                                                                                                                                                                                               153 LTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSNTQ 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 STSG-----SPDANGKENI------ASFMES-YVEQIKENKKLDT--- 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 --TYAGTAEIKQPVVKSLLDSKGIHYNQGNPYNLLTPVIEKVKPGEQSFVGQHAATGCVA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 IEVYLTT---KOPVVKSLLDSKGIHYNQGNPYNLLTPVIEKVKPGEQSFVGQHAATGCVA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFAAISTRQYNWNNILPTYSGRES 329
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                                                                                                                                                                                                                                                                                             39; Gaps
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                                                                                                                                                                                                                               Query Match 53.0%; Score 1324.5; DB 14; Length 398; Best Local Similarity 71.7%; Pred. No. 1.7e-90; Matches 273; Conservative 20; Mismatches 49; Indels 39;
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APPLICANT: Olmsted, Stephen
APPLICANT: Zagursky, Robert
APPLICANT: Wickbarg, Biliot
APPLICANT: Winchery Elliot
TITLE OF INVENTION: SURFACE PROTEINS OF STREPTOCOCCUS PYOGENES
FILE REFERENCE: AM 100399
CURRENT APPLICATION NUMBER: US/10/474,792
CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 674
SOFTWARE: Patentin version 3.0
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Publication No. US20040236072A1
GENERAL INFORMATION:
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                                                                                     ORGANISM: Artificial sequence
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Best Local Similarity
Matches 257; Conserval
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SEQ ID NO 24
LENGTH: 398
TYPE: PRT
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LENGTH: 398
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US-10-428-817A-164
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ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              400
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                   121 VSIDGIQSLSFDIETNKKAVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                    300
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                                                                                                                                                                                                    NHPKNLFAAISTRQYNWNNILPTYSGRESNVQKWAISELMADVGISVDMDYGPSSGSAGS 360
                                                                                                                                                                                                                                                                                                       361 SRVQRALKENFGYNQSVHQINRSDFSQDWEAQIDKELSQNQPVYYQGGKVGGHAFVIDGA 420
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                                                                                    181 SFWFDFFFPEPEFTQSKYLMIYKDNETLDSNTQIEVYLTTKQPVVKSLLDSKGIHYNQGNP
                                                                                                                                                      241 YNLLTPVIEKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYP
                                                                                                                                                                                                                                                                     SRVQRALKENFGYNGSVHOINRSDFSQDWEAQIDKELSQNQPVYYQGGKVGGHAFVIDGA
                                                                   SEWFDFFPEPEFTQSKYLMIYKDNETLDSNTQIEVYLTTKQPVVKSLLDSKGIHYNQGNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: mutant streptococcal pyrogenic exotoxin-B
US-10-002-784A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERRICE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 25
LENGTH: 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.3%; Score 1332; DB 14;
100.0%; Pred. No. 2.4e-91;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
US-10-002-784A-25
Sequence 25, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 53.3%
Best Local Similarity 100.0°
Matches 248; Conservative
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TITLE OF INTERTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE;
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE;
CURRENT APPLICATION NUMBER: US, 10/428, 817A
CURRENT FILING DATE: 2003-05-05
FRIOR PELING DATE: 2002-06-08
FRIOR FILING DATE: 2002-06-15
FRIOR APPLICATION NUMBER: US 60/389,366
FRIOR PELING DATE: 2002-06-15
FRIOR PELING DATE: 2002-06-15
FRIOR APPLICATION NUMBER: US 60/406,697
FRIOR FILING DATE: 2002-06-28
FRIOR PELING DATE: 2002-06-29
FRIOR PELING DATE: 2002-06-29
FRIOR PELING DATE: 2002-0-0-1
FRIOR FILING DATE: 2002-0-0-1
FRIOR FILING DATE: 2002-10-0-1
FRIOR FILING DATE: 2002-10-0-2
FRIOR FILING DATE: 2003-01-0-2
FRIOR FILING DATE: 2003-01-0-3
FRIOR FILING DATE: 2003-01-0-
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CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/682,431; 09/144,776
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
Sequence 164, Application US/10428817A Publication No. US20040214783A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24, Application US/10002784A Publication No. US20030036644A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Streptococcus pyogenes US-10-428-817A-164
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APPLICANT: Ulrich, Robert G.
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Sequence 27, Appl
Sequence 25, Appl
Sequence 164, Appl
Sequence 642, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 26, Appl
Sequence 16, Appl
Sequence 16, Appl
                                                                                                                      September 17, 2005, 00:44:58; Search time 145.152 Seconds (without alignments) 1305.574 Million cell updates/sec
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                                                                                                                                                                                                                                                   1 MQQDPDPSQLHRSSLVKNLQ......ALGTGGGAGGFNGYQSAVVG 468
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1: \cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: \cgn2_6/ptodata/2/pubpaa/PCT_MBW_PUB_pep:*

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5: \cgn2_6/ptodata/2/pubpaa/USO7_NBW_PUB_pep:*

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8: \cgn2_6/ptodata/2/pubpaa/USO8_NBW_PUB_pep:*

9: \cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

10: \cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

11: \cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-002-784A-25
US-10-002-784A-24
US-10-002-784A-24
US-10-474-792-642
US-10-474-792-642
US-10-872-198-25
US-11-021-951-25
I US-11-021-951-25
I US-08-882-431-16
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Maximum Match 100%
Listing first 45 summaries
                                                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                                                                          US-10-002-784A-27
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Query
Match Length D
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sequence 16, Appl Sequence 163, Appl Sequence 13, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 12, Appl Sequence 12, Appl Sequence 10, Appl Sequence 10, Appl Sequence 6, Appli Sequence 6, Appli Sequence 10, Appl Sequence 11, Appl Sequence 14, Appl Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 18, Appli Sequence 12, Appli
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APPLICANT: Ulrich, Robert G.
TILE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT APPLICATION NUMBER: 08/10/31; 09/144,776
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
7 US-10-767-687-16

6 US-10-428-817A-163

US-09-308-830-13

US-09-308-830-13

US-09-308-830-13

US-09-30-759-20

US-09-751-708A-20

US-09-150-947B-12

US-10-32-948-2

US-10-32-948-2

US-10-32-948-2

US-10-32-948-2

US-10-32-948-2

US-10-32-948-2

US-10-151-35-8

US-10-151-35-8

US-10-151-35-8

US-10-002-784A-6

US-10-002-784A-10

US-10-002-784A-10

US-00-882-431-10

US-00-2784A-14

US-10-002-784A-14

US-10-10-27-84A-14

US-10-10-27-84A-14

US-10-10-27-84A-14

US-10-10-27-84A-14

US-10-10-27-84A-14

US-10-10-27-34A-14

US-10-10-27-34A-14

US-10-10-27-34-4

US-10-10-23-324-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-751-708A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
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Best Local Similarity
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    SEQ ID NO 27
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58 KLKTELKNOEMATLFKDKNIDIYGVEYYHLCYLCENA-----ERSACI-GGVTNRE 107
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                                                                                                                                                                                                                       18;
                                                                                                                                                                        Query Match 21.6%; Score 541; DB 1; Length 255; Best Local Similarity 47.7%; Pred. No. 1.1e-39; Matches 113; Conservative 39; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: September 17, 2005, 00:48:31 Job time: 27.0362 secs
                                            : 255 amino acids
amino acid
INFORMATION FOR SEQ ID NO:
                     SEQUENCE CHARACTERISTICS LENGTH: 255 amino acio
                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-918A-2
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       GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/09/708,008B
CURRENT FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US/08/896,933
PRIOR FILING DATE: 1994-06-02
PRIOR FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 220
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Patent No. 5705151
GENERAL INFORMATION:
APPLICANT: Blmslie, Robyn E.
TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
UNMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,918A
FILING DATE: 18 - MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1700 Lincoln Street, Sulte 3500 CITY: Denver STATE: Colorado COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 552
ATTORNEY/AGENT INFORMATION:
NAME: KOVATIA, JOSEPH E.
REGISTRATION NUMBER: 23,005
REFERENCE/DOCKET NUMBER: 2879-29
TELEPHONE: (303) 863-920
TELEPHONE: (303) 863-023
                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-708-008B-20
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Best Local Similarity 84.99
Matches 185; Conservative
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64 NQEMATLFKDKOVDIYGVEYYHLCYLCENAERSACLYGGVTNHEGNHLEIPKKIVVKVSI 123
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                                   PDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKTELK
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Patent No. 6338845
GENERAL INFORMATION:
APPLICANT: Terman. David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
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Pred. No. 5.5e-75;
5; Mismatches 25;
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CURRENT APPLICATION NUMBER: US/09/314,235

CURRENT FILING DATE: 1999-05-10

EARLIER APPLICATION NUMBER: 08/252,978

EARLIER FILING DATE: 1997-07-18

EARLIER FILING DATE: 1994-06-02

EARLIER FILING DATE: 1991-01-17

EARLIER FILING DATE: 1990-01-17

EARLIER FILING DATE: 1990-01-17
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US-09-708-008B-20
; Sequence 20, Application US/09708008B
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Best Local Similarity 84.9%;
Matches 185; Conservative
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US-09-314-235-20
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                                                                                                                                                   Sequence 13, Application US/08973391C
Patent No. 6532441
GENERAL INFORMATION:
APPLICANT: Schlievert, Patrick M.
APPLICANT: Stoler, Jennifer
APPLICANT: Stoler, Jennifer
APPLICANT: Stoler, Jennifer
APPLICANT: Stoler, Jennifer
APPLICANT: Oblendorf, Jennifer
APPLICANT: Jennifer
A
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APPLICANT: Terman, David S.
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS, TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/996,933
CURRENT FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER APPLICATION NUMBER: 08/252,978
SARLIER APPLICATION NUMBER: 08/252,978
SARLIER FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FRASER FOR WINDOWN VERSION 3.0
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181 SFWFDFFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 221
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Best Local Similarity 97.3%;
Matches 215; Conservative
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LENGTH: 251
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APPLICANT: Terman, David S.

TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERATIGENS, AND RELATED COMPOUNDS
FILE REFERENCE: 09629/005004

CURRENT APPLICATION NUMBER: 08/09/314,235

CURRENT FILING DATE: 1999-05-18

EARLIER PILING DATE: 1999-06-18

EARLIER PELICATION NUMBER: 08/252,978

EARLIER PELICATION NUMBER: 08/252,978

EARLIER PELICATION NUMBER: 07/891,718

EARLIER PELICATION NUMBER: US91-00-17

EARLIER PELING DATE: 1992-06-01

EARLIER PILING DATE: 1991-01-17

EARLIER PILING DATE: 1990-01-17

EARLIER PILING DATE: 1990-01-17

EARLIER PELICATION NUMBER: 07/466,577

EARLIER PILING DATE: 1990-01-17

EARLIER PELING DATE: 1990-01-17

EARLIER PELING DATE: 1990-01-17

EARLIER PELING DATE: 1980-01-03

NUMBER OF SEQ ID NOS: 34

COOTUMARE: FREESO FOR WINDOWS 34
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                                         181 SFWFDFFFFFFTQSKYLMIYKDNETLDSNT-QIEVYLTTK 220
                                                                  SFWFDLFPEPEFTQSKYLMIYKONETLDSNTSQIEVYLTTK 221
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                                                                                                                                                                                           Sequence 29, Application US/09314235 Patent No. 6338845
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Best Local Similarity 97.3
Matches 215; Conservative
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APPLICANT: Schlievert, Patrick M.
APPLICANT: Schlievert, Patrick M.
APPLICANT: Schlievert, Jennifer
APPLICANT: Stocht, Jennifer
APPLICANT: Oblendorf, Douglas
TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
FILE REFERENCE: 600.311208 DS 793,391C
CURRENT APPLICATION NUMBER: US/08/973,391C
CURRENT FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: US 08/480,261
PRIOR PLLING DATE: 1996-06-07
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
SEQ ID NO 14
SEQ ID NO 14
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Pred. No. 2.6e-91;
1; Mismatches 3;
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Pred. No. 3.2e-91;
1; Mismatches 3;
PRIOR FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 29
LENGTH: 221
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Best Local Similarity 97.3%;
Matches 215; Conservative
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Best Local Similarity 97.3%;
Matches 215; Conservative
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62 ELKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: TERMIN, David S.

TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FABELSEQ for Windows Version 3.0
SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFWFDFFPEPEFTQSKYLMIYKDNETLDSNT-QIEVYLTTK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 SFWFDEPFEPEFTGSKYLMIYKDNETLDSNTSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1136; DB 4;
Pred. No. 2.2e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 29, Application US/08896933
Patent No. 6221351
GENERAL INFORMATION:
                                        NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Streptococcus pyogenes US-08-896-933-29
                                                                                                                                                                                                                                                                                                                                                                                                                                     45.4%;
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 98.2°
Matches 217; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 215; Conservative
                                                                                                                                                                                                                                                                                                       Unknown
                                                                                                                                                                                                                                                                                                                            TOPOLOGY: Unknown; MOLECULE TYPE: Peptide US-08-882-431B-16
                                                                                                                                                                                                                                                 LENGTH: 251
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-896-933-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
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| Sequence 16, Application US/0882431B
| Patent No. 6713284
| GENERAL INFORMATION:
| APPLICANT: Robert G. Ulrich,
| APPLICANT: Sina Bavari
| TITLE OF INVENTION: Bacterial Superantigen
| TITLE OF INVENTION: Bacterial Superantigen
| TITLE OF INVENTION: Vaccines
| NUMBER OF SEQUENCES: 25
| CORRESPONDENCE ADDRESS:
| ADDRESSEB: Charles H. Harris
| STREET: US Army MRWC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
| CITY: FORT DETRICK
| STREET: US Army MRWC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
| CUNTRY: USA | ADDRESSEB: COMPUTER: READABLE FORM:
| MEDIUM TYPE: Ploppy disk | COMPUTER: Apple Macintosh | SOFTWARE: Microsoft Word 6.0 |
| CURRENT APPLICATION NUMBER: US/08/882,431B |
| FILING DATE: Unne 25, 1997 |
| CLASSIFTARION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 ELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 ELKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.4%; Score 1136; DB 3; Length 251; 98.2%; Pred. No. 2.2e-92; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEWFDFFPEPEFTQSKYLMIYKDNETLDSNT-QIEVYLTTK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 SFWFDFFPEPEFTQSKYLMIYKDNETLDSNISQIEVYLTTK 251
                FILING DATE: 01-58p-1998
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: «Unknown»
ATTONEY, AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REGISTRATION NUMBER: 34,616
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
APPLICATION NUMBER: US/09/144,776B
                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 98.2
Matches 217; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: Ju
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REGISTRATION NUMBER: 32,750
REPERBENCH JOOGEN BAYL-004/02US
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 926-6200
ITELEPHONE: (415) 946-3713
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
PRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/09144776B Patent No. 6399332 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 25
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                                                                                                                                                                                                                              LENGTH: 398 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN: MGAS 1719 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US96-05997-1
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US-09-144-776B-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Misser M.D., James M.
APPLICANT: Kapur M.D., vivek
APPLICANT: Ananthaswamy, H. N.
APPLICANT: Ananthaswamy, H. N.
APPLICANT: Fernandez, A.
TITLE OF INVENTION: Use of extracellular cysteine protease
TITLE OF INVENTION: Use of inhibit cell proliferation
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEIL, GOTSHAL & MANGES
STREET: 2882 Sand Hill Road, Suite 280
CITY: Menlo Park
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                           Query Match 53.1%; Score 1327.5; DB 5; Length 398; Best Local Similarity 91.5%; Pred. No. 5.1e-109; Matches 258; Conservative 5; Mismatches 8; Indels 11;
AUTHORS: Hamrick, M. R.

AUTHORS: Hamil, R. J.

AUTHORS: Patti, J. M.

AUTHORS: Patti, J. M.

ITILE: A Conserved Streptococcus pyogenes

ITILE: extracellular cysteine protease cleaves

ITILE: fibronectin and degrades vitronectin

VOLUME: 15

VOLUME: 15

PARES: 327-346

PATE-US95-11723-5
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 01-MAY-1995
CLASSIFICATION:
PRICATION DATA:
APPLICATION NUMBER: US 08/306,542
FILING DATE: 14-SEP-1994
FILING DATE: 18-SEP-1994
APPLICATION NUMBER: US 08/160,965
FILING DATE: 02-DEC-1993
ATTOMING DATE: 02-DEC-1993
ATTOMING DATE: NAMME: Rae-Venter Ph.D., Barbara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMBER: PCT/US96/05997
01-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application PC/TUS9605997 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rae-Venter Ph.D., Barbara
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174 EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGIKDYTYTLSSNNPYFNHPKNLFA 233
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                                                                                                                                                                                                                                                                              249 EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 AISTROYNWANILPTYSGRESNVORMAISELMADVGISVDMDYGPSSGSAGSSRVORALK 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294 ENFGYNQSVHQINRSDFSKQDWEAQIDKELSQNQPVYYQGVGKVGGHAFVIDGADGRNFY 353
                                                                                                                                                                                      120 PMES-YVEQIKENKKLDT----TYAGTAEIKQPVVKSLLDSKGIHYNQGNPYNLTTPVI
                                                                                                                                         192 FTOSKYLMIYKDNETLDSNTQIEVYLTT---KQPVVKSLLDSKGIHYNQGNPYNLLTPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369 ENFGYNQSVHQINRSDFS-QDWEAQIDKELSQNQPVYYQG-GKVGGHAFVIDGADGRNFY
                                                                         Gaps
                                                                             11;
          DB 5; Length 398;
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ADDRESSE: Charles H. Harris
STREET: US Army MRMC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
Query Match 53.1%; Score 1327.5; DB 5
Best Local Similarity 91.5%; Pred. No. 5.1e-109;
Matches 258; Conservative 5; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Bacterial Superantigen Vaccines
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ORGANISM: Streptococcus pyogenes
STRAIN: MGAS 1719
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLONE: SPEB7 (cysteine protease)
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Topouzis, S.
Majesky, M. W.
Li, L. L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 398 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
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Patent No. 6833262
GENERAL INFORMATION
FILENCEMATION: A POLYPEPTIDE HAVING AMIDOLYTIC ACTIVITY FOR A SERPIN FILE REFERENCE: 215.0021.0201
CURRENT APPLICATION NUMBER: US/10/030,330
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: 60/130,436
PRIOR APPLICATION NUMBER: 60/130,436
PRIOR APPLICATION NUMBER: 60/130,436
PRIOR SEQ ID NOS: 6
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO S. 6
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 FTOSKYLMIYKDNETLDSNTQIEVYLTT---KOPVVKSLLDSKGIHYNQGNPYNLLTPVI
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                                                                                                                                                                                                                                                                                                                                                                                      Query Match 53.1%; Score 1327.5; DB 3; Length 398; Best Local Similarity 91.5%; Pred. No. 5.1e-109; Matches 258; Conservative 5; Mismatches 8; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.1%; Score 1327.5; DB 4; Length 398; 91.5%; Pred. No. 5.1e-109.
                                                                   AUTHORS: Kapur, V.
AUTHORS: Topouzis, S.
AUTHORS: Majesky, M. W.
AUTHORS: Li, L.- L.
AUTHORS: Hamil, R. J.
AUTHORS: Hamil, R. J.
AUTHORS: Maser, J. M.
AUTHORS: Muser, J. M.
AUTHORS: Muser, J. M.
TITLE: A conserved Streptococcus pyogenes
TITLE: Atracellular cysteine protease cleaves human
TITLE: fibronectin and degrades vitronectin
JOURNAL: Microb. Pathog.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 5.1e-109; 5; Mismatches 8;
STRAIN: MGAS 1719
MEDIATE SOURCE:
CLAONE: SPER7 (cysteine protease)
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Streptococcus pyogenes
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Matches 258; Conservative
                                                                                                                                                                                                                                                                                                            ; PAGES: 327-346
; DATE: 1993
US-08-931-220-5
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ENFGYNOSVHOINRSDFS-QDWEAQIDKELSQNOPVYYOG-GKVGGHAFVIDGADGRNFY 426
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BEATENIN Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: PCT/US95/11723
FILING DATE: 14-SEP-1995
CLASSIFICATION NUMBER: US 08/306,542
FILING DATE: 14-SEP-1994
ATTORNEY/AGENIN INFORMATION:
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: 32,750
REFERENCE/DOCKET NUMBER: 32,750
RELEPHONE: (415) 956-6205
TELEPHONE: (415) 956-6205
TELEPHONE: (415) 956-6205
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                              RESULT 3
PCT-US99-11723-5
Sequence 5, Application PC/TUS9511723
GENERAL INFORMATION:
APPLICANT: Muser M.D., James M.
TITLE OF INVENTION: Methods and Compositions for TITLE OF INVENTION: Methods and Compositions for SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAW OFFICES OF BARBARA RAE-VENTER STREET: P.O. BOX 60039
CITY: Palo Alto
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us-10-002-784a-27.rai

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USA
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                                                                   September 17, 2005, 00:42:17; Search time 26.0362 Seconds (without alignments) 1341.817 Million cell updates/sec
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Sequence 8, Appli
Sequence 14, Appl
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                                                                                                                                     1 MQQDPDPSQLHRSSLVKNLQ.....ALGTGGGAGGFNGYQSAVVG 468
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Sequence 16,
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/bcTUS_COMB.pep:*
        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-030-330-6
PCT-US95-11723-5
PCT-US96-0597-1
US-09-144-7766-16
US-08-882-431B-16
US-09-314-235-29
US-09-314-235-29
US-09-373-391C-13
US-08-973-391C-13
US-08-974-176B-6
US-08-882-431B-6
US-09-144-776B-16
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US-08-896-933-26
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US-09-144-776B-14
                                                                                                                                                                                          513545 segs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
                                                OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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Match Length
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; Patent No. 6030835
; GENERAL INFORMATION:
    APPLICANT: Muser M.D., James M.
    APPLICANT: Aguer M.D., Vivek
    TITLE OF INVENTION: Methods and Compositions for Identifying
    TITLE OF INVENTION: Group A Streptococcus
    NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: WEIL, GOTSHAL & MANGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
FILING DATE: US 08/306,542
FILING DATE: US 08/160,965
FILING DATE: US 08/100,965
FILING DATE: US
US-08-882-431B-14
US-08-896-933-28
US-09-108-008B-28
US-09-708-008B-28
US-09-314-235-27
US-09-314-235-27
US-09-314-235-21
US-09-314-235-21
US-09-314-235-21
US-09-314-335-21
US-09-114-776B-24
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US-09-114-776B-24
US-09-882-431B-24
US-08-882-431B-24
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US-09-316-235-25
US-09-316-235-25
US-08-446-918A-4
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STREET: 2882 Sand Hill Road, Suite 280
CITY: Menlo Park
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INFORMATION FOR SEQ ID NO: 5:
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LENGTH: 398 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 FTQSKYLMIYKDNETLDSNTQIEVYLTT----KQPVVKSLLDSKGIHYNQGNPYNLLTFVI 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 XISTRQYNWNNILPTYSGRESNVQKMAKSELMADVGISVDMDXXPSSGSAGSSRVQRALX 293
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                                                                                                                                                                                                                                       Novel oral bacterial periodontain polypeptide for treating periodontal diseases, has amidolytic activity for cleavage of non-denatured human alphal-proteinase inhibitor at reactive site loop region of inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.8%; Score 1195.5; DB 3; Length 398; 84.0%; Pred. No. 1.3e-88; ive 5; Mismatches 29; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HVNWGWGGVSDGFEHLDALNPSALGTGGGAGGFNGYOSAVXG 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 468
                                                                    (UYGE-) UNIV GEORGIA RES FOUND INC.
(FARAV) TRAVIS J.
(POTE/) POTEMPA J.
(NELS/) NELSON D.
                                                                                                                                                                                                                                                                                                                 Example 1; Fig 1; 55pp; English
                                                                                                                                                                  Nelson
20-APR-2000; 2000WO-US010574.
                                   99US-0130436P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 84.0
Matches 237; Conservative
                                                                                                                                                                Fravis J, Potempa J,
                                                                                                                                                                                                   WPI; 2000-679600/66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 398 AA;
                                   21-APR-1999;
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Search completed: September 17, 2005, 01:09:43 Job time : 154.962 secs

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hyperimmune serum reactive antigen or its fragment from Streptococcus pyogenes. The nucleic acid molecule or hyperimmune serum-reactive antigen or its fragment are useful for the manufacture of a pharmaceutical preparation, especially a vaccine, against S. pyogenes infection. In addition, the hyperimmune serum reactive antigen or fragment is used for the isolation and/or purification and/or identification of an interaction partner of the hyperimmune serum reactive antigen or its fragment, for the generation of a poptide (e.g. anticalines) binding to the antigen or fragment, or for the manufacture of a functional nucleic acid selected from aptements and spiegelmers. The nucleic acid molecule may also be used for the manufacture of functional ribonucleic acids such as ribozymes, antisense nucleic acids and siRNA. ADR83733-ADR84189 represent S. pyogenes hyperimume serum reactive antigens, fragments and the encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AISTROYNWINILPTYSGRESNVOKMAISELMADVGISVDMDYGPSSGSAGSSRVQRALK 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid molecules encoding hyperimmune serum-reactive antigens from Streptococcus pyogenes, useful for diagnosing, preventing and treating S. pyogenes infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTQSKYLMIYKDNETLDSNTQIEVYLTT----KQPVVKSLLDSKGIHYNQGNPYNLLTPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENFGYNQSVHQINRSDFS-QDWEAQIDKELSQNQPVYYQG-GKVGGHAFVIDGADGRNFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S. pyogenes mature pyrogenic exotoxin B (SpeB) mutant protein (C47S)
                                                                                                                             invention describes a novel nucleic acid molecule encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.9%; Score 1323.5; DB 8; Length 398; larity 91.1%; Pred. No. 4.6e-99; Conservative 5; Mismatches 9; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Superantigen toxin; vaccine; infection; pyrogenic exotoxin B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Wild type Cys substituted with Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 468
                                                                                                                                                                                                                                                                                                                                                                                                 polynucleotide described in the invention
                                                                                        Claim 14; SEQ ID NO 239; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE37690 standard; protein; 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
tes 257; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 398 AA;
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Matches
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10-JUL-2003

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61 YPNKGLKDYTYTLSSNNPYFNHPKNLFAAISTRQYMWNILPTYSGRESNVQKWAISELM 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           460
                                                                                                                                                                                                                                                         The invention provides a superantigen toxin DNA fragment which has been genetically altered such that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is disrupted or altered. DNA fragments of the invention are useful in the production of vaccines against bacterial superantigen toxin infections. They are also useful in gene therapy. The present sequence is Streptococcus pyogenes mature pyrogenic exotoxin B (SpeB) mutant protein. This sequence is used in the invention. Note: This sequence is not shown in the specification, but is derived from S. pyogenes mature wild-type SpeB protein (AAB37686)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                             New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pyogenes; streptopain; periodontain; antiinflammatory; antibacterial; amidolytic; alpha_l-proteinase inhibitor; periodontitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 ADVGISVDMDYGPSSGSAGSSRVQRALKENFGYNQSVHQINRSDFSQDWEAQIDKELSQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QPVYYQGGKVGGHAFVIDGADGRNFYHVNWGWGGVSDGFFRLDALNPSALGTGGGGGFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QPVVKSLLDSKG1HYNQGNPYNLLTPV1EKVKPGEQSFVGQHAATGSVATATAQIMKYHN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221 QPVVKSLLDSKGIHYNQGNPYNLLTPVIEKVKPGEQSFVGQHAATGCVATATAQIMKYHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADVGI SVDMDYGPSSGSAGSSRVQRALKENFGYNQSVHQINRSDFSQDWEAQIDKELSQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QPVYYQGGKVGGHAFV1DGADGRNFYHVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1322; DB 7;
Pred. No. 3.1e-99;
                                                                              (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB36098 standard; protein; 398 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pyogenes streptopain.
                                                                                                                                                                                                                            Claim 42; Page; 141pp; English.
               26-NOV-2001; 2001WO-US046540
                                             26-NOV-2001; 2001US-00002784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 99.6
Matches 247; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYQSAVVG 468
                                                                                                                                              WPI; 2003-492125/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 248 AA;
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                                                                                                                Ulrich RG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity. [1], nucleic acids encoding [1], ABN66044-ABN71526 and antibodies that bind [1] are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding [1] are used to detect Streptococcus in a biological sample. [1] is used to determine whether a compound binds to used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding [1] may be used to recombinantly produce [1] and may be used in gene therapy. Antibodies to (1) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                          EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA 308
                                                                                                                                                                                                                                                                                                                                                                                                                   AISTROYNWNNILPTYSGRESNVOKWAISELMADVGISVDMDYGPSSGSAGSSRVQRALK 368
antibacterial and antiinflammatory
                                                                                                                                                                                                                                                                                                   FTQSKYLMIYKDNETLDSNTQIEVYLTT---KQPVVKSLLDSKGIHYNQGNPYNLLTPVI
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                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                            DB 5; Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pyogenes pyrogenic exotoxin B (SpeB) protein
                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 468
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                                                                                                                                                                                                                                                           Pred. No. 4.6e-99;
                                                                                                                                                                                                                                            Score 1323.5;
                                                                                                                                                                                                                                                                       5; Mismatches
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/label= Signal_peptide
146. .398
specification. The proteins have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                          52.9%;
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                                                                                                                                                                                                                                                                       Matches 257; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pyogenes.
                                                                                                                                                                                   Streptococcus proteins
                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                               Sequence 398 AA;
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                                                                                                                                                                                                                                                                                                                                                                           EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA 233
                                                                                                                                                                                                                                                                                                                                                                                                                      426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention provides a superantigen toxin DNA fragment which has been genetically altered such that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is disrupted or altered. DNA fragments of the invention are useful in the production of vaccines against bacterial superantigen toxin infections. They are also useful in gene therapy. The present sequence is Streptococcus pyogenes pyrogenic exotoxin B (SpeB) protein. This sequence is used in the
                                             superantigen toxin DNA fragment, useful for preparing a composition treating or preventing bacterial infection.
                                                                                                                                                                                                                                                                                                                     AISTRQYNWNNILPTYSGRESNVQKWAISELMADVGISVDMDYGPSSGSAGSSRVQRALK
                                                                                                                                                                                                                                                                                                                                                        EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENFGYNQSVHQINRSDFS-QDWEAQIDKELSQNQPVYYQG-GKVGGHAFVIDGADGRNFY
                                                                                                                                                                                                                                                                                                     FTQSKYLMIYKDNETLDSNTQIEVYLTT---KQPVVKSLLDSKGIHYNQGNPYNLLTPVI
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                      DB 7; Length 398;
                                                                                                                                                                                                                                                                             9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        serum reactive antigen; vaccine; anticaline.

    S. pyogenes hyperimmune system reactive antigen Spy2039.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 468
                                                                                                                                                                                                                                                      Score 1323.5; DB Pred. No. 4.6e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gelbmann D;
                                                                                                                                                                                                                                                                             5; Mismatches
                                                                                   Example 14; Page 133; 141pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; protein; 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nagy E, Winkler B,
                                                                                                                                                                                                                                                      52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAR-2004; 2004WO-EP002087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-MAR-2003; 2003EP-00450061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                               Matches 257; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INTE-) INTERCELL AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-653698/63.
N-PSDB; ADR83821.
                         WPI; 2003-492125/46.
                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                            Sequence 398 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004078907-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hyperimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-SEP-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Meinke A,
RG
                                                                                                                                                                                                      invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADR83971;
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                                                                                                                                                                                                                                                      Query Match
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Ulrich
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ABP29579;
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ABP29579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pyrogenic enterotoxin a; vaccine; superantigen toxin; MHC; superantigen-associated bacterial infection; bacterial infection; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              superantigen toxin DNA fragment, useful for preparing a composition treating or preventing bacterial infection.
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                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pyrogenic toxin b, wild-type pro-sequence,
                                   HILLER HILLER HILLER HILLER HAVING HA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 14; Page 40-42; 68pp; English.

    .145
    /label= Pro_peptide
    146. .398
    /label= Mature_SPEb

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                                                                                                                                                                                                                   ABU62332 standard; protein; 398 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-00882431,
98US-00144776,
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                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 398 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JUN-1997;
01-SEP-1998;
                                                                                                                                                                                                                                                                                                                                               27-AUG-2003
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                                                354
427
                                                                                                                                                                                                                                                                                 ABU62332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Peptide
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Gaps

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388
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                                                                                                                                                                                                               329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
95 ERSACI-GGVTNREGNHLEIPKKIVVKVSIDGIQSLSPDIETNK-KMVTAQELDYKVRKY 152
                                                                                                                                                                                                                                                                                                                   314
                                                                                                                                                                                                                                                                                                                                                        447
                                                                                                                                                                                                                                                                                                                                                                                     315 WEAQIDKELSQNQPVYYQGVGKVGGHAFVIDGADGRNFYHVNWGWGGVSDGFFRLDALNP 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Streptococcus protein for the treatment or prevention of infection disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
                                                                   153 LIDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSNTQ
                                                                                         137 --TYAGTAEIKQPVVKSLLDSKGIHYNQGNPYNLLIPVIEKVKPGEQSFVGGHAATGCVA
                                                                                                                                                                                                                             195 TATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFAAISTRQYNWNNILPTYSGRES
                                                                                                                                                                                                                                                                                                     255 NVQKWAISELMADVGISVDMDYGPSSGSAGSSRVQRALKENFGYNQSVHQINRGDFSKQD
                                                                                                                                                                                                                                                                                                                                                    389 WEAQIDKELSQNQPVYYQG-GKVGGHAFVIDGADGRNFYHVNWGWGGVSDGFFRLDALNP
                                                                                                                                       213 IEVYLTT----KOPVVKSLLDSKGIHYNQGNPYNLLTPVIEKVKPGEQSFVGQHAATGCVA
                                                                                                                                                                                                             270 TATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFAAISTRQYNWNNILPTYSGRES
                                                                                                                                                                                                                                                                                  NVQKWAISELMADVGISVDMDYGPSSGSAGSSRVQRALKENFGYNQSVHQINRSDFS-QD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Masignani V, Margarit Y RosI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus polypeptide SEQ ID NO 8334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 3948; 4525pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            375 SALGTGGGAGGFNGYQSAVVG 395
                                                                                                                                                                                                                                                                                                                                                                                                                          SALGTGGGAGGFNGYQSAVVG 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP29579 standard; protein; 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-OCT-2001; 2001WO-GB004789.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-352536/38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Telford J,
Tettelin H;
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enterotoxin; cytostatic; gene therapy; cancer;

Streptococcal pyrogenic exotoxin B (SpEB) sequence.

(first entry)

26-FEB-2004

ADF89840;

Superantigen; SAg; enterotoxir pyrogenic exotoxin; SpE; SpEB.

Streptococcus sp.

WO2003094846-A2

20-NOV-2003

15-JUN-2002; 2002US-0389366P. 28-AUG-2002; 2002US-0406697P. 29-AUG-2002; 2002US-040550P. 01-0CT-2002; 2002US-0415310P. 02-OCT-2002; 2002US-0415400P.

09-JAN-2003; 2003US-0438686P.

(TERM/) TERMAN D S.

WPI; 2004-011997/01.

Terman DS;

08-MAY-2003; 2003WO-US014381.

2002US-0378988P.

08-MAY-2002;

us-10-002-784a-27.rag

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                                                                                                                                                                                                                                                                                                                             This sequence represents the S. pyogenes cysteine protease speb7. The invention relates to a method for determining the presence of a Group A Street which expresses an extracellular protease (preferably speb8) capable of degrading proteins of the extracellular matrix, comprising:

(1) combining a sample with an assay medium comprising a first member of a specific binding pair which binds to a second member of the binding pair which binds to a second member of the binding pair to form a complex, where the first member not the protease; competitive with at least 1 conserved epitopic site on the protease; and (2) detecting complex formation as indicative of the presence of the patence of infection with Streptococcus pyogenes and for monitoring the disease status of the host. The speB gene products are used as a vaccine for protecting against Streptococcus mediated diseases such as for protecting against Streptococcus mediated diseases such as parting the companion of the monitoring and acute theumatic fever, sepsis, erysipelas, fascilitis, pneumonia, acute rheumatic fever, sepsis, erysipelas, fascilitis, pneumonia, acute rheumatic fever, sepsis, and
                                                                                                                                                                                                                                                    Determining the presence of a Group A Streptococcus expressing a protease capable of degrading proteins of the extracellular matrix, using a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AISTRQYNWNNILPTYSGRESNVQRWAISELMADVGISVDMDYGPSSGSAGSSRVQRALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FMES-YVEQIKENKKLDT----TYAGTAEIKQPVVKSLLDSKGIHYNGGNPYNLLTPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AISTROYNWNNILPTYSGRESNVQKMAISELMADVGISVDMDYGPSSGSAGSSRVQRALK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FTQSKYLMIYKDNETLDSNTQIEVYLTT---KQPVVKSLLDSKGIHYNGGNPYNLLTPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.1%; Score 1327.5; DB 3; Length ilarity 91.5%; Pred. No. 2.2e-99; Conservative 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 468
                                                                                                                                                                                                                                                                                                      Disclosure, Col 7-8; 56pp; English.
                                                                                                                                                      BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                93US-00160965.
94US-00306542.
                                                                                         97US-00931220
                                                                                                                                                                                   Musser JM;
                                                                                                                                                                                                            WPI; 2000-205208/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 258; Conserv
                                                                                                                                                                                                                                                                               specific antibody.
                                                                                                                                                                                                                         N-PSDB; AAA07111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 398 AA;
                                                                                       16-SEP-1997;
                                                                                                                  02-DEC-1993;
                                                                                                                              14-SEP-1994;
                                     US6030835-A.
                                                              29-FEB-2000
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                                                                                                                                                                                   Kapur V,
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The invention relates to treating a subject with cancer. The method involves administering an amount of a superantigen (SAg) composition comprising a molecule selected from: a native SAg protein; its biologically active fragment or a biologically active homologue or a biologically active fusion protein comprising the SAg or its fragment or homologue fused to a fusion partner polypeptide or peptide. The SAg is selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic exotoxin, Y. pseudotuberculosis SAg, Mycoplasma arthritides SAg and Clostridium perfringens exotoxin. The method is useful in treating cancer or malignant diseases such as malignant pleural effusion, ascites,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248
Treating a subject with cancer or malignant diseases comprises intratumoral, intrathecal or intracavitary administration of an amount of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353
                                                                                                                                                                                                                                                                                                                                                                                                                represents a Streptococcal pyrogenic exotoxin B (SpEB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 FMES-YVEQIKENKKLDT----TYAGTAEIKOPVVKSLLDSKGIHYNGGNPYNLLTPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 FTQSKYLMIYKDNETLDSNTQIEVYLTT---KQPVVKSLLDSKGIHYNQGNPYNLLTPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 8; Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1327.5; DB 8; Delis-
Pred, No. 2.2e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
                                                    superantigen composition to the subject.
                                                                                                        Disclosure; SEQ ID NO 17; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.1%;
91.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 258; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 398 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249
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HVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 395

354

ADF89840 standard; protein; 398

ADF89840 ID ADF8 RESULT 9

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The present sequence is the Streptococcus pyogenes clone speB7 pre-pro cysteline protease (CP), which can be used to inhibit neoplastic cell proliferation, especially in a human, useful in the treament of neoplastic conditions, e.g. carcinomas, sarcomas, melanomas, lymphomas and leukaemias originating from blood, lung, mammary gland, prostate, intestine, stomach, liver, heart, skin, pancreas or brain tissue. The CP is especially associated with a wound covering, and can also be used to prevent metastasis or identify susceptible neoplastic cells, K1735 and CM519 melanoma cells were injected s.c. into nu/nu mice, optionally followed by i.p. injection of CP (100 microg, 24 hours later). The mice were checked twice weekly for tumour growth for 12 weeks, to give results that showed that treatment with CP completely protected athymic mice against transplanted K195 melanoma growth, and protected 60% of the mice
                                                                                                                                                                                                                                                                                                                                                                                          248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody; vaccine; diagnosis; detection; Streptococcus infection; group A; prevention; treatment; pharyngitis; tonsillitis; skin infection; acute rheumatic fever; scarlet fever; probe; post-streptococcal glomerulonephritis; sepsis; meningitis; erysipelis;
                                                                                                                                                                                                                                                                                                                                                                                                              EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 AISTRQYNWNNILPTYSGRESNVQKWAISELMADVGISVDMDYGPSSGSAGSSRVQRALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FTQSKYLMIYKDNETLDSNTQIEVYLTT---KQPVVKSLLDSKGIHYNQGNPYNLLTPVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENFGYNQSVHQINRSDFS-QDWEAQIDKELSQNQPVYYQG-GKVGGHAFVIDGADGRNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenic peptide; speB gene; extracellular protease; production;
                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                     DB 2; Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           333. 338
/label= putative nucleotide binding domain
382. 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= potential collagen docking region
                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S. pyogenes speB gene encoded extracellular protease.
                                                                                                                                                                                                                                                                                                                S3.1%; Score 1327.5; DB 2; Similarity 91.5%; Pred. No. 2.2e-99; 8; Conservative 5; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cellulitis; fasciitis; toxic shock like syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "corresponding codon TAG" 333. .338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR95856 standard; protein; 398
                                                                                                                                                                                                                                                from developing CM519 melanomas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                   Sequence 398 AA;
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Best Local Simi
Matches 258;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-0CT-1996
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21-MAR-1996

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The present sequence is the S. pyogenes speB gene encoded extracellular protease. An immunogenic peptide derived from the protease can be used in the prodn. of antibody (Ab) and vaccine. Ab is prepd. by introducing the peptide into a mammal, pref. a mouse, followed by Ab isolation. The Ab or a probe derived from the gene can be used for the diagnosis and detection of gp. A Streptococcus infections, while vaccine, which inhibite streptococcus infections, and be used to prevent and treat gp. A Streptococcus infections, acute rheumatic fever, scallet fever, streptococcus infections, acute rheumatic fever, scallet fever, streptococcus glomerulonophritis, sepsis, meningitis, erysipelis, cellulitis, fascitts and toxic shock like syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248
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                                                                                                                                                                                                              Use of extracellular protease(s), partic. cysteine protease - for detection, diagnosis prevention and treatment of infection by pathogenic organisms, partic. gp. A streptococcus strains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cysteine protease; speB; Group A Streptococcus; extracellular protease; detection; diagnosis; extracellular matrix; infection; skin infection; disease status monitoring; vaccine; Streptococcus mediated disease; pharyngitis; tonsillitis; scarlet fever; sepsis; erysipelas; fasciitis; pneumonia; acute rheumatic fever; poststreptococcal glomerulonephritis; cellulitis; bacteraemia; meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 AISTROYNWINILIPTYSGRESNVORMAISELMADVGISVDMDYGPSSGSAGSSRVORALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294 ENFGYNQSVHQINRSDFSKQDWEAQIDKELSQNQPVYYQGVGKVGGHAFVIDGADGRNFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTQSKYLMIYKDNETLDSNTQIEVYLTT ---KQPVVKSLLDSKGIHYNQGNPYNLLTPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S. pyogenes cysteine protease speB7 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HVNWGWGGVSDGFFRLDALNPSALGTGGGGGGGFNGYQSAVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .2e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.1%; Score 1327.5; 91.5%; Pred. No. 2.2e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Mismatches
                                                                                                                                                                                                                                                                                       Disclosure; Page 12; 97pp; English.
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                                                                                   (BAYU ) BAYLOR COLLEGE MEDICINE.
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                95WO-US011723
                                                    94US-00306542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 91.5
Matches 258; Conservative
                                                                                                                          Kapur V;
                                                                                                                                                          WPI; 1996-179944/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 398 AA;
                                                                                                                                                                           N-PSDB; AAT15294
                                                14-SEP-1994;
                13-SEP-1995;
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Length 248; Indels

53.3%; Score 1332; DB 7; L 100.0%; Pred. No. 4.7e-100; iive 0; Mismatches 0;

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Disclosure; Page 59-61; 99pp; English
                                                        Matches 248; Conservative
                                            Similarity
             Sequence 248 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1995;
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                                   Query Match
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                                                                                                            QPVVKSLLDSKGIHYNQGNPYNLLTPVIEKVKPGEQSFVGQHAATGCVATATAQIMKYHN 280
                                                                                                                                                                    61 YPNKGLKDYTYTLSSNNPYFNIPKNLFAAISTRQYNWANILPTYSGRESNVQKMAISELM 120
                                                                                                                                                                                                               YPNKGLKDYTYTLSSNNPYFNHPKNLFAAISTRQYNWNNILPTYSGRESNVQKMAISELM 340
                                                                                                                                                                                                  ADVGISVDMDYGPSSGSAGSSRVQRALKENFGYNQSVHQINRSDFSQDWEAQIDKELSQN 400
                                                                                                                                                                                                                                               OPVYYQGGKVGGHAFVIDGADGRNFYHVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFN 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention provides a superantigen toxin DNA fragment which has been genetically altered such that binding of the encoded altered toxin to either the MHC class II or I cell antigen receptor is disrupted or altered. DNA fragments of the invention are useful in the production of vaccines against bacterial superantigen toxin infections. They are also useful in gene therapy. The present sequence is Streptococcus pyogenes mature pyrogenic exotoxin B (SpeB) protein. This sequence is used in the invention
                                                                                                                                  9
SPEb). The superantigen toxin DNA fragment is useful for preparing a composition for treating or preventing bacterial infection. The present sequence represents the wild-type SPEb mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.
                                                                                                                           1 QPVVKSLLDSKGIHYNQGNPYNLLTPVIEKVKPGEQSFVGQHAATGCVATATAQIMKYHN
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superantigen toxin; vaccine; infection; pyrogenic exotoxin B; SpeB;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pyogenes mature pyrogenic exotoxin B (SpeB) protein.
                                                                                       ;
                                                                  Length 248;
                                                                53.3%; Score 1332; DB 7; Length 2
100.0%; Pred. No. 4.7e-100;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (USME-) US MEDICAL RES INST INFECTIOUS DISEASES
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                                                                                                                                                                                                                                                                                                                                                                      AAE37686 standard; protein; 248 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-NOV-2001; 2001WO-US046540
                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                          Local Similarity 100.
Les 248; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                           468
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                                                                                                                                                                                                                                                                                           GYQSAVVG
                                            Sequence 248 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene therapy.
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                                                                 Query Match
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Matches
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280
                                                                                                                                           61 YPNKGLKDYTYTLSSNNPYFNHPKNLFAAISTRQYNWNNILPTYSGRESNVQKMAISELM 120
                                                                                                                                                                                                                            400
                                                                                                                                                                                                                                                                460
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                                                  9
                                                                                                              YPNKGLKDYTYTLSSNNPYFNHPKNLFAAISTRQYNWNNILPTYSGRESNVQKMAISELM
QPVVKSLLDSKGIHYNQGNPYNLLTPV1EKVKPGEQSFVGQHAATGCVATATAQIMKYHN
                                               1 OPVVKSLLDSKGIHYNQGNPYNLLTPVIEKVKPGEQSFVGQHAATGCVATATAQIMKYHN
                                                                                                                                                                                                                               advgi svdmdygpssgsagssrvoralkenfgynosvho inrsdfsodweao idkelson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of extracellular Streptococcal cysteine protease enzyme - for inhibiting the proliferation of neoplastic cells, e.g. for treating carcinoma, lymphoma or leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pyogenes clone speB7 pre-pro cysteine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fernandez A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 333. .338
/label= nucleotide_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "corresponding codon TAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ananthaswamy H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW07898 standard; protein; 398 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BAYU ) BAYLOR COLLEGE MEDICINE. (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96WO-US005997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-00432692,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GYQSAVVG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GYOSAVVG 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Musser JM, Kapur V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-506148/50.
N-PSDB; AAT45219.
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Misc-difference
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SFWFDFFPEPEFTQSKYLMIYKDNETLDSNTQIEVYLTTKQPVVKSLLDSKGIHYNQGNP
                        181
                                                       241
                                                                                                               301
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                                                                                                                                                                                                                                                                                                                               ABU62333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELKNQEMATLFKOKNIDIYGVEYYHLCYLCENAERSACIGGVTNREGNHLEIPKKIVVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSIDGIQSLSFDIETNKKAVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MQQDPDFSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQRRSHDLIYNVSGPNYDKLK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention provides a superantigen toxin DNA fragment which has been genetically altered such that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is disrupted or altered. DNA fragments of the invention are useful in the production of vaccines against bacterial superantigen toxin infections. They are also useful in gene therapy. The present sequence is Streptococcus pyogenes mature mutant pyrogenic exotoxin A (SpeA)-mature mutant SpeB fusion protein. This sequence is used in the invention. Note: This sequence is not shown in the specification, but is derived from S. pyogenes mature wild-type SpeA-SpeB protein (AAE37684)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               superantigen toxin DNA fragment, useful for preparing a composition treating or preventing bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                       Superantigen toxin; vaccine; infection; pyrogenic exotoxin A; SpeA; gene therapy; fusion protein; SpeB; mutant; mutein.

    S. pyogenes mature mutant SpeA-mature mutant SpeB fusion protein.

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                                                                                                                                                                                                                                                                                              /note= "Wild type Leu substituted with Arg"
                                                                                                                                                                                                                                                                                                                                       /note= "Wild type Cys substituted with Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.4e-193;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.4%; Score 2484; DB 7; 99.6%; Pred. No. 1.4e-193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
                                                                                                                                                                                                                                                                             'note= "Encoded by GCT"
                                                                                                                                                                                                                                                Location/Qualifiers
                                   AAE37691 standard; protein; 468 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 14; Page; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                             26-NOV-2001; 2001WO-US046540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-NOV-2001; 2001US-00002784
                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 99.6
                                                                                                                                                                                                    Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-492125/46.
                                                                                                                                                                                                                                                                                           Misc-difference 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 468 AA;
                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                      WO2003056015-A1
                                                                                              06-0CT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ulrich RG;
                                                                                                                                                                                                                  Synthetic
                                                                 AAE37691;
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Matches
         RESULT 3
                       AAE3769
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fragment is altered so that binding of the encoded altered toxin DNA fragment is altered so that binding of the encoded altered toxin to either the MHZ class II or T cell antigen receptor is altered. Also included are a recombinant DNA construct (comprising a vector and an isolated and purified altered superantigen toxin DNA fragment), a host cell transformed with the recombinant DNA construct, producing altered superantigen toxin, peptide, diagnosing superantigen-associated bacterial superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin) superantigen toxin peptide, diagnosing superantigen-associated bacterial infection, a vaccine (comprising an altered superantigen toxin for producing antigenic and immunogenic response resulting in the protection of a mammal against superantigen-associated bacterial infection, treating/ameliorating a superantigen-associated bacterial infection, an antisera isolated from individuals immunised with one or more altered TSST-1 superantigen toxin and an antibody which recognises altered TSST-1. Also disclosed are mutated staphylococcal enterotoxin a and b (SPEa and SEB) SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and
                                                                                                                                     360
                                                       300
                                                                                             300
                                                                                                                                                                           360
                                                                                                                                                                                                                      420
                                                                                                                                                                                                                                         toxin; MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.
SFWFDFFFBEFFTQSKYLMIYKDNETLDSNTQIEVYLTTKQPVVKSLLDSKGIHYNQGNP
                                                                            241 YNLITPVIEKVKPGEQSFVGQHAATGSVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYF
                                                                                                                                                               301 NHPKNLFAAISTRQYNWNNILPTYSGRESNVQKMAISELMADVGISVDMDYGPSSGSAGS
                                                     YNLLTPVIEKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYF
                                                                                                                                     NHPKNLFAAISTROYNWNNILPTYSGRESNVOKMAISELMADVGISVDMDYGPSSGSAGS
                                                                                                                                                                                                                    SRVQRALKENFGYNQSVHQINRSDFSQDWEAQIDKELSQNQPVYYQGGKVGGHAFVIDGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pyrogenic enterotoxin a; vaccine; superantigen toxi superantigen-associated bacterial infection; bacterial infection;
                                                                                                                                                                                                                                                                                                        468
                                                                                                                                                                                                                                                                                                                         Streptococcus pyrogenic toxin b, wild-type mature sequence.
                                                                                                                                                                                                                                                                                                    DGRNFYHVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 14; Page 42-43; 68pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU62333 standard; protein; 248
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98US-00144776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2003036644-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-AUG-2003
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exotoxin

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TELKNÓEMATLFKDKNIDIYGVEYYHLCYLCENAERSACIGGVTNREGNHLEIPKKIVVK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRVQRALKENFGYNQSVHQINRSDFSQDWEAQIDKELSQNQPVYYQGGKVGGHAFVIDGA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention provides a superantigen toxin DNA fragment which has been genetically altered such that binding of the encoded altered toxin to either the WHC class II or T cell antigen receptor is disrupted or altered. DNA fragments of the invention are useful in the production of vaccines against bacterial superantigen toxin infections. They are also useful in gene therapy. The present sequence is Streptococcus pyogenes pyrogenic exotoxin A (SpeA)-SpeB fusion protein. This sequence is used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   superantigen toxin DNA fragment, useful for preparing a composition treating or preventing bacterial infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 YNLJTPVIEKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELKNQEMATLFKDKNID1YGVEYYHLCYLCENAERSAC1GGVTNREGNHLE1PKKIVVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YNLLTPVIEKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NHPKNLFAAISTROYNWNNILPTYSGRESNVOKWAISELMADVGISVDMDYGPSSGSAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRVQRALKENFGYNQSVHQINRSDFSQDWEAQIDKELSQNQPVYYQGGKVGGHAFVIDGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MOODPDPSQLHRSSLVKNLONIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 2500; DB 7;
100.0%; Pred. No. 6.9e-195;
iive 0; Mismatches 0;
                       infection; pyrogenic
                                                                                                                                                                                                                                                                                                              (USME-) US MEDICAL RES INST INFECTIOUS DISEASES
                     Superantigen toxin; vaccine; infect
gene therapy; fusion protein; SpeB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 10; Page 134; 141pp; English
                                                                                                                                                                                                                     26-NOV-2001; 2001WO-US046540.
                                                                                                                                                                                                                                                                 26-NOV-2001; 2001US-00002784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                      Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-492125/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAD56778
                                                                                                                              WO2003056015-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the invention
                                                                                                                                                                          10-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                     Ulrich RG;
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                                The invention relates to an isolated and purified superantigen toxin DNA fragment is altered so that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is altered. Also included are a recombinant DNA construct, producing a vector and an isolated and purified altered superantigen toxin DNA fragment), a host cell transformed with the recombinant DNA construct, producing altered superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin) or superantigen toxin peptide, diagnosing superantigen-associated bacterial infection, superantigen toxin for producing antigenic and immunogenic response resulting in the protection of mammal against superantigen-associated bacterial infection, an antisera isolated from individuals immunised with one or more altered TSST-1 superantigen toxin and an antibody which recognises altered TSST-1. Also disclosed are mutated staphylococcal enterotoxin A, B, Cl (SEA, SEB, SEL) and streptococcal pyrogenic enterotoxin A, B, Cl (SEA, SEB). The superantigen toxin and an antibody which recognises altered TSST-1. Also disclosed are mutated staphylococcal enterotoxin A, B, Cl (SEA, SEB). The superantigen toxin DNA fragment is useful for preparing a composition for treating or preventing bacterial infection. The present CC sequence represents the SPEB LAZR/SPEB C475 mutant fusion protein. Note: The present sequence is described as having the Cys to Ser mutation in the residue is still Cys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSIDGIQSLSPDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE
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; Pred. No. 6.9e-195;
0; Mismatches 0;
Claim 10; Page 44-46; 68pp; English
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Best Local Similarity 100.
Matches 468; Conservative
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Streptococcus pyogenes SpeA-SpeB fusion protein.

RESULT 2 AAE37684

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Aaw1206 7
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Aaw59799 Aaw5979 Aaw59799 Aaw5979 Aaw5979 Aaw5979 Aaw5979 Aaw5979 Aaw5979 Aaw59

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New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.
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Misc-difference 100. .101

Misc-difference 211. .212

Misc-difference 386. .387

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/note= "Encoded by GGTGTCGGT"
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                                            AAR45017
ABB76240
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AAW51254
AAW12154
AAW12146
AAW12147
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AAW5979
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WPI; 2003-492125/46.
N-PSDB; ACD28908.
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01-SEP-1998;
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Aar95886 S. pyogen
Aay81812 S. pyogen
Abu62332 Streptoco
Aba57685 Streptoco
Aae37690 S. pyogen
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Abu62334 Streptoco
Aae37689 S. pyogen
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Abu2333 Streptoco
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Abu2260 Streptoco
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Aae37691 S. pyogen
Abu62333 Streptoco
Aae37686 Streptoco
                                                                                                     September 17, 2005, 00:47:53; Search time 152.962 Seconds (without alignments) 1183.322 Million cell updates/sec
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2500
1 MQDPDFSQLHRSSLVKNLQ......ALGTGGGAGGFNGYQSAVVG 468
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           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                     2105692 seqs, 386760381 residues
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Listing first 45 summaries
                                                                         OM protein - protein search, using sw model
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AAW07898
AAR95856
AAY81812
ADF89840
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ABU10088
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Gapop 10.0 , Gapext 0.5
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geneseqp2000s:*
geneseqp2001s:*
geneseqp2003as:*
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: geneseqp1980s:*
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No.
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US ATTEN MANG -504 Scott Street MCWR-JA (Charles H. Harris-
CITY: FORT DETRICK
STATE: MARYLAND
COUNTY: USA
ZIP: 21702-5012
COMPUTER: READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: Apple Macintosh 7.5
SOFTWARE: Miscintosh 7.5
SOFTWAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 TRHYLVKNKKLYEFNNSPYETGYIKFI-ENENSFWYDMMPAPGDKFAQSKYLMMYNDNKM 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
42.9%; Score 567.5; DB 4; Length 266;
Best Local Similarity 47.5%; Pred. No. 1.8e-46;
Matches 121; Conservative 40; Mismatches 75; Indels 19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250 vĎSKDVKIEVÝĽTTK 264
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STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-882-431B-6
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US-09-144-776B-6
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US-08-882-431B-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 KVTAOELDYLTRHYLVKNKKLYEFNNSPYETGYIKFI-ENENSFWYDMMPAPGDKFDOSK 239
                     169 MVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEP--EFTQSK 226
--ERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 THENVKSVDQLRSHDLIYNVSGP---NYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 YLCENA-----ERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SHILISHVILIFALILVISTPNVLAESQPDPKPDELHKSSKFTGLMENMKVLYDDNHV 60
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mason, Hugh
APPLICANT: Palmer, Kenneth
APPLICANT: Palmer, Kenneth
APPLICANT: Hefferon, Kathleen
APPLICANT: Mor, Tsafrir
APPLICANT: Arntzen, Charles
TITLE OF INVENTION: Genain Virus Vectors for Gene Expression in Plants
TITLE OF INVENTION: Genain Virus Vectors for Gene Expression in Plants
CURRENT APPLICATION NUMBER: US/09/414,276
VORRENT APPLICATION NUMBER: US/09/414,276
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 LKKMVFF---VLVTFLGLTIS-QEVFA--QQDPDPSQLHRSSLVKNL-QNIYFLYEGDPV
                                                                       182 YLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNETLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78; Indels
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43.5%; Score 575; DB 3;
Best Local Similarity 47.2%; Pred. No. 3.5e-47;
Matches 125; Conservative 40; Mismatches 78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Bacterial Superantigen Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 YLMMYNDNKMYDSKDVKIEVYLTTK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 YLMIYKDNETLDSNTSQIEVYLTTK 251
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                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09414276
Patent No. 6392121
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: bean yellow dwarf virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                   240 NTSQIEVYLTTK 251
                                                                                                                                                                                       242 KDVKIEVYLTTK 253
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LENGTH: 266
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71 LRSHDLIYNVSGP---NYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCENA---- 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 VRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNET 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 TRHYLVKNKKLYBFNNSPYETGYIKFI-ENENSFWYDMMPAPGDKFAQSKYLMMYNDNKM 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 VLVTFLGLTIS-QEVFA--QQDPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
ADDRESSEE: Charles H. Harris
STREET: US Army MRMC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 42.9%; Score 567.5; DB 3; Best Local Similarity 47.5%; Pred. No. 1.8e-46; Matches 121; Conservative 40; Mismatches 75;
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Sequence 6, Application US/08882431B
Sequence 6, Application US/08882431B
Sequence 6, Application Sequence 6, Ulrich,
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                       COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REPERENCE/DOCKET NUMBER: <UNK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
                                                                                                                                                                          ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (301) 619-7714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 266
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250 VDSKDVKIEVYLTK 264
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                                                                                                  CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
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182 YLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFPPEP--EFTQSKYLMIYKDNETLDS 239
                                                                                                                                                                                                                                                                                 183 YLVKNKKLYEFNNSPYETGYIKFI-ENENSFWYDMMPAPGDKFDQSKYLMMYNDNKAVDS 241
                                                                                     74 HDLIYNVSGP---NYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCENA----- 123
                                                                                                                                                                        124 --ERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRK 181
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      15 VLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVDQLRS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 VLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVDQLRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 HDLIYNVSGP---NYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCENA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08580806
Patent No. 5935568
GENERAL INFORMATION:
APPLICANT: Dow, Steve W.
APPLICANT: Elmslie, Robyn E.
APPLICANT: Potter, Terence A.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 13
CORRESPENDENCE Sheridan Ross & McIntosh
STRRET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,806
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFRENCE/DOCKET NUMBER: 2879
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                            240 NTSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                                                  242 KDVKIEVYLTIK 253
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ZIP: 80203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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US-08-580-806-2
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Best Local 9
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                                                                                                                                                                                                                                                                                 4 PKPSQLQRSNLVKTFKIYIFFWRVTLVTHENVKSVDQLLSHDLIYNVSGPNYDKLKTELK 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08446918A
Patent No. 5705151
GENERAL INFORMATION:
APPLICANT: Elmslie, Robyn E.
TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,918A
FILING DATE: 18-MAY-1995
CLASSIFICATION: 552
ATTORNEY/AGENT INFORMATION:
NAME: KOVARIK, JOSEPH E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2879-29
TELEPHONE: (303) 863-970
TELEPHONE: (303) 863-970
TELEPHONE: (303) 863-923
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
TYPE: amino acid
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                                                                                                                                                                                                                24;
                                                                                                                                                                        DB 4;
                                                                                                                                                                  74.1%; Score 979.5; DB 4
86.7%; Pred. No. 3.7e-86;
tive 4; Mismatches 24
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NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                              TYPE: PRT ORGANISM: Streptococcus pyogenes
                                                                                                                                                               Query Match
Best Local Similarity 86.74
Matches 189; Conservative
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CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
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US-08-446-918A-2
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                                     SEQ ID NO 20
LENGTH: 220
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TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE FILE REFERENCE: 600.311USWO
CURRENY PAPPLICATION NUMBER: US/08/973,391C
CURRENY FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: PCT/US96/10252
PRIOR PILING DATE: 1996-06-07
PRIOR PILING DATE: 1996-06-07
PRIOR PILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 14
LENGTH: 221
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Pred. No. 8.7e-104;
0; Mismatches 2; Indels
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TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOKINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS;
FILE REPRENENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 20
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Pred. No. 3.7e-86;
4; Mismatches 24
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; Sequence 20, Application US/08896933
? Patent No. 6221351
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                          , ORGANISM: Streptococcus pyogenes US-08-973-391C-14
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US-08-896-933-20
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Best Local Similarity 99.1%;
Matches 219; Conservative (
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Best Local Similarity 86.7
Matches 189; Conservative
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94 NQEMATLEKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVKVSI 153
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; Sequence 20, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
    APPLICANT: TErman, David S.
    TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
    TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
    TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
    TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
    CURRENT APPLICATION NUMBER: US/09/708,008B
    CURRENT FILING DATE: 2000-11-08
    PRIOR PILING DATE: 1997-07-18
    PRIOR PILING DATE: 1997-07-18
    PRIOR PILING DATE: 1994-06-02
                                                                                                                                                                                                                                                                                   APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
FILE REFERENCE: 06629/005004
CURRENT APPLICATION NUMBER: US/09/314,235
CURRENT FILING DATE: 1999-05-18
EARLIER FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 06/85,933
EARLIER FILING DATE: 1994-06-02
EARLIER FILING DATE: 1994-06-01
EARLIER FILING DATE: 1991-01-17
EARLIER PILING DATE: 1991-01-17
EARLIER APPLICATION NUMBER: 07/466,577
EARLIER PILING DATE: 1990-01-17
EARLIER FILING DATE: 1990-01-17
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183 FDFFPEPEFTQSKYLMIYKONETLDSNTSQIEVYLTTK 220
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Pred. No. 3.7e-86;
4; Mismatches 24
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 20
LENGTH: 220
                                                                                                                                                                                   Sequence 20, Application US/09314235; Patent No. 6338845; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               i ORGANISM: Streptococcus pyogenes
US-09-314-235-20
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Best Local Similarity 86.7
Matches 189; Conservative
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US-09-708-008B-20
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61 ELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 120
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                                                                             31 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 29, Application US/09708008B

Patent No. 6692746

GENERAL INFORMATION:
APPLICAMT TERMAN. David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS;
FILE REFERENCE: 09629/005002;
CURRENT APPLICATION NUMBER: US/09/708,008B

CURRENT FILING DATE: 2000-11-08

PRIOR APPLICATION NUMBER: US/08/896,933

PRIOR FILING DATE: 1997-07-18

PRIOR PLICE DATE: 1994-06-02
     99.1%; Pred. No. 7e-104;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    181 SFWFDLFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 221
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                                                                                                                                                                                                                                                                                                                                                                         211 SFWFDFFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 251
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
US-08-973-391C-14
Sequence 14, Application US/08973391C
Setence 14, Application US/08973391C
Retent No. 663241
GENERAL INFORMATION:
APPLICANT: SCHIevert, Patrick M.
APPLICANT: Stocht, Jennifer
APPLICANT: Ohlendorf, Douglas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Streptococcus pyogenes
US-09-708-008B-29
                              219; Conservative
Best Local Similarity
Matches 219; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
US-09-708-008B-29
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LENGTH: 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 VSIDGIQSLSFDIETNKANVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 210
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TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERAWRIGENS, AND RELATED COMPOUNDS
FILE REFERENCE: 09629/005004
CURRENT APPLICATION NUMBER: US/09/314,235
CURRENT FILING DATE: 1999-05-18
EARLIER APPLICATION NUMBER: 08/896,933
EARLIER FILING DATE: 1997-07-18
EARLIER FILING DATE: 1994-06-02
EARLIER FILING DATE: 1994-06-01
EARLIER FILING DATE: 1991-01-17
EARLIER APPLICATION NUMBER: 07/486,577
EARLIER FILING DATE: 1991-01-17
EARLIER FILING DATE: 1990-01-17
EARLIER FILING DATE: 1990-01-03
NUMBER OF SEQ ID NOS: 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                       APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS, TITLE OF INVENTION: SUPERANTICENS, AND RELATED COMPOUNDS FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
EARLIER PILING DATE: 1997-07-18
EARLIER PILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FASEC for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFWFDFFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 251
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                      Sequence 29, Application US/08896933
Patent No. 6221351
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 29, Application US/09314235
Patent No. 6338845
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-896-933-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.13
Matches 219; Conservative
                                                                                                                                                                                                                                                                                                                      SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-314-235-29
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LENGTH: 221
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Geguence 13, Application US/08973391C
Fatent No. 6632441
GENERAL INFORMATION:
APPLICANT: Schlievert, Patrick M.
APPLICANT: Schein, Manuela
APPLICANT: Scoein, Manuela
APPLICANT: Scoein, Manuela
APPLICANT: Scoein, Manuela
APPLICANT: Oliendorf, Douglas
TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
FILE REFERENCE: 600.311USMS: US/08/973,391C
CURRENT APPLICATION NUMBER: US/08/973,391C
CURRENT FILING DATE: 1999-03-12
FRIOR APPLICATION NUMBER: US 08/480,261
FRIOR FILING DATE: 1996-06-07
FRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 14
SOGTWARRE: Patentin version 3.1
                                                                                                                               61 THENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC 120
                                                                                                                                                                                            ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVR 180
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                                             1 MENNKKYLKKWYFFVLVTFLGLIISQEVFAQQDPDFSQLHRSSLVKNLQNIYFLYEGDPV
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98.9%; Score 1308; DB 4;
Best Local Similarity 99.2%; Pred. No. 1.2e-117;
Matches 249; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CRGANISM: Streptococcus pyogenes
US-08-973-391C-13
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Sequence 16 Application US/08882431B

Patent NO. 6713284

GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Sina Bavari

TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS: 25
CORRESPONDENCE ADDRESS: 35
COUNTY: FORT DETRICK
STATE: MARYLAND
COUNTY: USA
STATE: MARYLAND
COUNTY: USA
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
OPERATING SYSTEM: Macintosh
OPERATING SYSTEM: Macintosh
OPERATION DATA:
MAPPLICATION NUMBER: US/08/882,431B
FILING DATE: June 25 1907
                                                                                                                                                                            61 THENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC 120
                                                                                                                                                                                                                                                              121 ENAERSACIYGGYTNHEGNHLEIPKKIVVKVSIDGIOSLSFDIETNKKMVTAQELDYKVR 180
                                                                                                                                                                                                                                                                                                                                                   181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSN 240
                                                                                                                                                   61 THENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC 120
                                                                                                                                                                                                                                        121 ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMYTAQELDYKVR 180
                                                                                                                                                                                                                                                                                                                            KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSN 240
                                                                                    1 MENNYKKYLKKAYPFYLYTFLGLIISQEVFAQQDPDFSQLHRSSLYKYLQNIYFLYEGDPV 60
                                                             1 MENNYKKVLKKMVFFVLVTFLGLTISQEVFAQQDPDFSQLHRSSLVKNLQNIYFLYEGDPV 60
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                    Indels
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1 Similarity 100.0%; Pred. No. 5.6e-119; 251; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: JUNE 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/POCKET NUMBER:
TELEPHONE: (391) 619-2065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-714
INPORMATION FOR SEQ ID NO: 16.
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 251; Conserv
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US-08-882-431B-16
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27, Appl 27, Appl 27, Appl 21, Appl 21, Appl 24, Appl 25, Appl 25, Appl 25, Appl 25, Appl 25, Appl 26, Appl 27, Appl 28, Appl 29, Appl 212, Appl 212,

Sequence Sequence Sequence

Sequence Sequence Sequence

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Perfect score:

9

Sequence:

Scoring table:

Searched:

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Length 251;
                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US ARMY MRMC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
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US-08-896-933-27
US-09-314-235-27
US-09-314-235-27
US-09-314-235-21
US-09-314-735-21
US-09-108-008B-21
US-09-114-776B-24
US-08-882-431B-24
US-08-882-431B-24
US-09-314-235-25
US-09-314-235-25
US-09-314-235-25
US-08-484-2238-112
US-08-484-2238-112
US-08-484-2238-112
US-08-485-551A-112
US-08-485-551A-112
                                                                                                                                                                                                                                                                                                                             APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Bloppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
RILING DATE: cUNKNOWN:
ATORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: 4UKNOWN:
TELECOMMUNICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 16:
18-09-144-776B-16
                                                                                                                                                                                                                                                                                           Sequence 16, Application US/09144776B Patent No. 6399332 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: Amino Acid
STRANDEDNESS: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPAX: (301) 619-7
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
 US-09-144-776B-16
  Query Match
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                                                                           September 17, 2005, 00:42:17; Search time 13.9638 Seconds (without alignments) 1341.817 Million cell updates/sec
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                                                                                                                                    1322
1 MENNYKKULKKMVPFVLVTFL.....KDNETLDSNTSQIEVYLTTK 251
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/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-965-913-29
US-08-973-3910-13
US-09-114-235-29
US-09-708-008B-29
US-08-99-313-20-14
US-09-314-235-20
US-09-314-235-20
US-09-446-918h-2
US-09-446-918h-2
US-09-414-776B-6
US-09-144-776B-6
US-09-144-776B-10
US-08-882-431B-10
US-08-886-331-26
US-09-144-776B-10
US-08-886-331-26
US-09-144-776B-10
US-08-886-331-26
US-09-314-235-26
US-09-314-235-26
US-09-314-235-26
US-09-144-776B-8
                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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-08-882-431B-14
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Maximum Match 100%
Listing first 45 summaries
                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Result No.

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8;
                                                                                                                                                          71 LRSHDLIYNVSG---PNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC--ENAER 125
                                                                                                                                                  15 VLVTFLGLTIS-QEVFAQQDPD--PSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVDQ 70
                                                                                                                      Query Match 41.7%; Score 551.5; DB 1; Length 266;
Best Local Similarity 46.1%; Pred. No. 3.2e-33;
Matches 117; Conservative 46; Mismatches 74; Indels 17; Gaps
                                                                                                                30671 MW; SED8A32D11FFCA59 CRC64;
Enterotoxin type C-3.
                                                                                                                                                                                  DSNTSQIEVYLTTK 251
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Search completed: September 17, 2005, 01:13:36 Job time : 82.5939 secs

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  129 GKVTGGKTCMYGGITKHEGNHFDNGNLQNVLIRVYENKRNTISFEVQTDKKSVTAQELDI 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 MVF-FVLVTFLGLTISQEVFAQQDPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSV
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                                                                                                                                                                 MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5; Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramateu K.; "Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     41.8%; Score 553; DB 2; Length 266;
44.5%; Pred. No. 2.5e-33;
tive 51; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 266 AA; 30670 MW; 4C654659AA48120F CRC64;
                                                                  Last annotation update)
                                                                                                  Staphylococcus aureus (strain MW2).
Bacteria, Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=196620;
                                                       sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
25-OCT-2004 (Rel. 45, Last annocation update)
Enterotoxin type C-3 precursor (SEC3).
Name=entC3; OrderedLocusNames=SAV2009, SA1817;
                                                                                                                                                                                                                              Lancet 359:1819-1827(2002).

EMBL; AP004824; BAB94624.1; -.

EMBL; AP004824; BAB94624.1; -.

EMSL; AP004824; BAB94624.1; -.

GO; GO:0005405; C:extracellular; IEA.

GO; GO:0009405; P:pathogenesis; IEA.

InterPro; IPR008052; Bact endotox.

InterPro; IPR008052; Bact endotox.

InterPro; IPR008123; Stap/Strep_toxin.

InterPro; IPR006123; Stap/Strep_toxin.

InterPro; IPR006123; Stap/Strep_toxin.

Pfam; PF01123; Stap_Strp_toxin.

Pfam; PF01123; Stap_Strp_toxin.

PROSITE; PR00279; STAPH_STREP_TOXIN_1; D:

PROSITE; PS00277; STAPH_STREP_TOXIN_2; 1.
                        266 AA.
                                          01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2003 (TrEMBLrel. 22, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
ENTERCYOXIN TYPE C.
Name-sec4; OrderedLocusNames=WW0759;
                     PRT;
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TVDSKRVKIEVHLTTK 264
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Matches 114; Conservative
                     PRELIMINARY;
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                                                                                                                                             SEQUENCE FROM N.A. STRAIN=MW2;
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SEQUENCE 266 AA;
                                                                                                                                                                                                                          acquired MRSA.";
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P23313;
01-NOV-1991
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                    OBNXJ6
RESULT 14
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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| R PDB; 1JCK; X-ray; B/D=28-266. |
| R PDB; 1JCK; X-ray; D=28-266. |
| R PDB; 1JWM; X-ray; D=28-266. |
| R PDB; 1JWM; X-ray; D=28-266. |
| R PDB; 1JWU; X-ray; D=28-266. |
| R PDB; 1KLG; X-ray; D=28-266. |
| R PDB; 1KLG; X-ray; D=28-266. |
| R PDB; 1KLG; X-ray; D=28-266. |
| R InterPro; 1PR006912; Bact endotox. |
| R InterPro; 1PR006123; Staph/Strept_toxin. |
| R InterPro; 1PR006123; Staph/Strept_toxin. |
| R InterPro; 1PR006123; Staph tox_OB. |
| R InterPro; 1PR006123; Staph tox_OB. |
| R InterPro; 1PR008123; Staph Strept_toxin. |
| R PR01123; Stap Strp_toxin; 1. |
| R PR01123; Stap Strp_toxin; 1. |
| R PR051TE; PS00279; BACTRLTOXIN. |
| R PR051TE; PS00279; STAPH_STREP_TOXIN. |
| R PR051TE; PS00278; STAPH_STREP_
                                                                                                                                                                                                                                                                                                                                                           STRAIN=Muso / ATCC 700699, and N315;

STRAIN=Muso / ATCC 700699, and N315;

STRAIN=Muso / ATCC 700699, and N315;

MEDLINE=21311952; Pubmed=11418146; DOI=10.1016/S0140-6736(00)04403-2;

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

Mizutani U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Howde C.J., Hackett S.P., Bohach G.A., "Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence comparison of all three type C staphylococcal enterotoxins."; Mol. Genet. 220:329-333(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 384:188-192 (1996).

-1- FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ø
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Secreted. SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH TCR.
Staphylococcus aureus (strain Mu50 / ATCC 700699),
Staphylococcus aureus (strain N315), and
                                                                                                                                                                          Bacteria, Firmicutes, Bacillales, Staphylococcus.
NCBI_TaxID=158878, 158879, 1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90220508; PubMed=2325627;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lancet 357:1225-1240(2001).
                                                                 Staphylococcus aureus. Staphylococcus aureus.
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249
        SHQTDKRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 DOLRSHDLIYNVSG---PNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC--ENA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 DKFLAHDLIYNISDKKLKNYDKVKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 ER----SACIYGGVTNHEGNHLEIPK--KIVVKVSIDGIQSLSFDIETNKKMVTAQELDY 177
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SEQUENCE FROM N.A.
MEDLINE=20566668; PubMed=11114901; DOI=10.1128/JB.183.1.63-70.2001;
Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
Meaney W.J., Smyth C.J.;
"Characterization of a putative pathogenicity island from bovine
Staphylococcus aureus encoding multiple superantigens.";
J. Bacteriol. 183:63-70(2001).
EMBL, AF217235; AAG225599.1; -.
HSSP; P34071; 114X.
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                                                                                             TRHYLVKNKKLYEFNNSPYETGYIKFI-ENENSFWYDMMPAPGDKFDQSKYLMMYNDNKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 MVF-FVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3493F6228B042F10 CRC64;
                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TEMBLrel. 25, Last annotation update)
Staphylococcal enterotoxin C-bovine.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus.
Bacteria, Firmicutes; Bacillales; Staphylococcus
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GO; GO:0009405; P:pathogenesis; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR000992; Bact_endotox.
InterPro; IPR0006123; Bact_endotox.
InterPro; IPR006123; Stap/Strept_tox.
InterPro; IPR006124; Stap/Strept_tox.
InterPro; IPR006125; Stap/Strept_tox.
InterPro; IPR006173; Stap/tox.03.
Pfam; PF01123; Stap Strp_tox.03.
Pfam; PF02876; Stap_Strp_tox.03.
PRINTS; RR00277; STAPH_STREP_TOXIN 1; 1.
PROSITE; PS00277; STAPH_STREP_TOXIN 2; 1.
SEQUENCE 271 AA; 31267 MW; 3493F6228B042
                                                                                                                                                                                                                                                                                                  271 AA
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TVDSKSVKIEVHLTTK 269
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VDSKDVKIEVYLTTK 264
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                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                              Name=sec-bov;
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DQFLYFDLI -> NBFFDLIYL (in Ref. 3).

Missing (in Ref. 3).

DIN -> NDD (in Ref. 3).

QTD -> ENT (in Ref. 3).

NG -> GN (in Ref. 3).

Y -> YY (in Ref. 3).

QE -> EQ (in Ref. 3).

QE -> EQ (in Ref. 3).

D -> N (in Ref. 3).

D -> N (in Ref. 3).
InterPro; IPR006126; Staph/Strept toxin.
InterPro; IPR006126; Staph/Strept tox.
InterPro; IPR006173; Staph.cox. OB.
Pfam; PF01276; Stap Strp tox C; 1.
Pfam; PF01123; Stap_Strp_toxin; 1.
PR0817F; PR00279; BACTRITOXIN 1.
PROSITE; PS00277; STAPH_STREP TOXIN 1; 1.
PROSITE; PS00276; STAPH_STREP_TOXIN 2; 1.
Superantigen; Toxin.
27
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266 AA;
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Matches 123; Conserv
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MEDLINE=85298255; PubMed=3898073;
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MEDILINESE6168029.
JOHNS C.L., Khan S.A., PubMed=3957869;
"Nucleotide sequence of the enterotoxin B gene from Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.7%; Score 1054; DB 2; Length 222; 89.2%; Pred. No. 8.4e-71;
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Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Bacteria: Firmicutes; Bacillales; Staphylococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Mismatches
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13-AUG-1987 (Rel. 05, Last seq
25-OCT-2004 (Rel. 45, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriol. 166:29-33(1986).
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SEQUENCE OF 40-91 FROM N.A.
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Matches 198, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    222 AA;
                                                                           SEQUENCE FROM N.A.
                                           NCBI_TaxID=1314;
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SEQUENCE
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Ranelli D.M., Jones C.L., Johns M.B., Mussey G.J., Khan S.A.;
"Molecular cloning of staphylococcal enterotoxin B gene in Escherichia
coli and Staphylococcus aureus ";
Proc. Natl. Acad. Sci. U.S.A. 82:5850-5854 (1985).
                                                                                                                                                                                                                                                                                                                Huang I.-Y., Bergdoll M.S.; "The primary structure of staphylococcal enterotoxin B. 3. The cyanogen bromide peptides of reduced and aminoethylated enterotoxin B, and the complete amino acid sequence."; J. Biol. Chem. 245:3518-3525(1970).
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MEDLINE=98181012; PubMed=9514739; DOI=10.1006/jmbi.1997.1577;
Papageorgiou A.C., Tranter H.S., Acharya K.R.;
Papageorgiou A.C., Tranter H.S., Acharya K.R.;
Crystal structure of microbial superantigen staphylococcal
enterotoxin B at 1.5-A resolution: implications for superantigen
recognition by MHC class II molecules and T-cell receptors.";
J. MOID Biol. 277:61-79(1998).
J. MOID Biol. 277:61-79(1998).
Staphylococcal enterotoxins cause the intoxication
staphylococcal food poisoning syndrome. The illness characterized
by high fever, hypotension, diarrhea, shock, and in some cases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93063291; PubMed=1436058; DOI=10.1038/359801a0; Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.; "Crystal structure of staphylococcal enterotoxin B, a superantigen."; Nature 359:801-806(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.
MEDLINE=94203282; PubMed=8152483; DOI=10.1038/368111a0;
Jardetzky T.S., Erven, J.H., Gorga J.C., Stern L.J., Urban R.G.,
Chi Y.I., Stauffacher C., Strominger J.L., Wiley D.C.;
"Three-dimensional structure of a human class II histocompatibility
molecule complexed with superantigen.";
Nature 368:711-718(1994).
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SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS)
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PDB; 15BB; X-ray; B/D=28-266.
PDB; 15B3; X-ray; B=28-266.
PDB; 15B4; X-ray; G=28-266.
PDB; 15B4; X-ray; D/H=29-262.
PDB; 25BB; X-ray; D/H=29-262.
PDB; 35BB; X-ray; G=28-266.
PDB; 35BB; X-ray; G=28-265.
InterPro; 1PR008992; Bact endotox.
InterPro; 1PR006177; Bctrl_tox.
                                                                                                                                                                                                                                                                               MEDLINE=71007902; PubMed=5470821;
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1D5X; X-ray; C=28-266.
1D5Z; X-ray; C=28-266.
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81 SGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNH 140
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K Ralia A. Bessen D.E.;

K Ralia A. Bessen D.E.;

T "Presence of streptococcal pyrogenic exotoxin A and C genes in human isolates of group G streptococci.";

FEMS Microbiol. Lett. 219:291-295 (2003).

B. MEBL; AY043745; AAL06668.1; -..

B. HSSP; PO1552; ISBB.

C GO: 00:0005576; C:extracellular; IEA.

BR GO; GO:000576; C:extracellular; IEA.

BR GO; GO:000576; P:pathogenesis; IEA.

BR InterPro; IPR006173; Bact endotox.

BR InterPro; IPR006123; Staph/Strept tox.

BR InterPro; IPR006123; Staph/Strept tox.

BR InterPro; IPR006125; Staph/Strept tox.

BR PROSTIS; Stap Strp tox C: 1.

BR PROSTIE; PS00279; BACTRLTOXIN.

BR PROSTIE; PS00277; STAPH_STREP_TOXIN.1; 1.
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                           LYTNGPSKYETGYIKFIPKNKESFWFDFFPBFFFTQSKYLMIYKDNETLDSNTSQI
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                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus equisimilis.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 AA; 25884 MW; 121F8460992818F8 CRC64;
                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Pyrogenic exotoxin A (Fragment)
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Last sequence update)
Last annotation update)
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89.2%; Pred. No. 8.4e-71;
ative 12; Mismatches 12;
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MEDLINE=22508029; Pubmed=12620634;
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
Exctoxin type A (Fragment).
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Matches 198; Conservative
                                                                                                                                                                                                  PRELIMINARY;
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GN Name=
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                                                                                                       129 IYGGVINHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQ 188
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DQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSAC 128
                                                                                                                                        69 DQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSAC 128
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WEDLINE=92044323; PubMed=1940804;

MELSON K., Schlievert P.M., Selander R.K., Musser J.M.;

MELSON K., Schlievert P.M., Selander R.K., Musser J.M.;

Characterization and clonal distribution of four alleles of the streptococcus pycogene. ";

T. Characterization and clonal distribution of four alleles of the streptococcus pycogenes.";

J. Exp. Med. 174:1271-1274(1991).

EMBL; X61573; CAA43771-11;

RSSP; P01552; LSBB.

GO; GO:0005576; C:extracellular; IEA.

RSSP; P01552; LSBB.

GO; GO:0005576; C:extracellular; IEA.

RO; GO:0009405; P:pathogenesis; IEA.

InterPro; IPR006123; Stap/Strept tox.

InterPro; IPR006123; Stap/Strept tox.

InterPro; IPR006124; Stap/Strept tox.

InterPro; IPR006125; Stap/Lox OB.

Pfam; PP01123; Stap Strp_tox OB.

PROSITE; PR00279; STAPH STREP_TOXIN_1; 1.

PROSITE; PROSITE; PROSITE; STAPH_STREP_TOXIN_1; 1.
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Best Local Similarity 88.6%; Pred. No. 7.1e-75;
Matches 209; Conservative 14; Mismatches 13; Indels
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Bacteria, Firmicutes, Lactobacillales; Streptococcaceae;
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236 AA; 27575 MW; 70F54120E79127DF CRC64;
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236
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222 AA;
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Hollingshead S.K., Beall B.;
"Genetic linkage of exotoxin alleles and emm gene markers for tissue
tropism in group A streptococci.";
T. Infect. Dis. 179:627-636(1999).
EMBL; AF055698; AAD11624.1; -.
PIR; A60108; A60108.
                                                                                                                                                                                                                                                                                                                   Gaps
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0
                                                                                                                                                                                                                                                                        Length 236;
                                                                                                                                                                                                                                                                                                                 2; Indels
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                         1 1 22 Potential.
23 >236 type A exotoxin.
236 236 AM, 2EF7F41AAC853600 CRC64,
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Last annotation update)
                                                                                                                                                                                                                                                                   Query Match
93.3%; Score 1234; DB 2;
Best Local Similarity 99.2%; Pred. No. 3.4e-84;
Matches 234; Conservative 0; Mismatches 2;
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GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005405; P:pathogenesis; IEA.

GO; GO:0009405; P:pathogenesis; IEA.

GO; GO:0009405; Bact endotox.

InterPro; IPR006177; Bctrl tox.

InterPro; IPR006126; Staph/Strept toxin.

InterPro; IPR006126; Staph/Strept toxin.

InterPro; IPR006126; Staph tox OB.

Pfam; PF01123; Stap Strp toxin; I.

PRMINTS: PR00279; BACTRITOXIN.

PROSITE; PS00277; STAPH_STREP_TOXIN 1; I.

PROSITE; PS00277; STAPH_STREP_TOXIN 2; I.

PROSITE; PS00277; STAPH_STREP_TOXIN 2; I.
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             Pfam; PF01123; Stap_Strp_Coxin; 1.
Pfam; PF02876; Stap_Strp_tox_C; 1.
PRNUTS; PR00279; BACTHIOXIN.
PROSITE; PS00277; STAPH STREP_TOXIN 1; 1.
PROSITE; PS002778; STAPH_STREP_TOXIN 2; 1.
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STRAIN=D709;
MEDLINE=99137798; PubMed=9952369;
InterPro; IPR006173; Staph_tox_OB
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01-MAY_2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
Exotoxin A (Fragment).
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NCBI_TaxID=1314;
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SEQUENCE
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                                                                                                                   Signal.
NON TER
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A Melson K., Schlevert P.M., Selander R.K., Musser J.M.;

T characterization and clonal distribution of four alleles of the speak

T gene encoding pyrogenic exotoxin A (scarlet fever toxin) in

Streptococcus pyrogenes.";

J. Exp. Med. 174:1271-1274(1991).

B RBL; Kels54; CAA43752.1;

GO; GO:0005576; Castracellular; IEA.

GO; GO:0005576; Castracellular; IEA.

R GO; GO:0005927; Brandogenesis; IEA.

InterPro; IPR006123; Stap/Strept.coxin.

InterPro; IPR006123; Stap/Strept.coxin.

InterPro; IPR006123; Stap/Atrept.cox.

InterPro; IPR006173; Stap. Lox. OB.

Pfam; PP01123; Stap_Strp_tox C; 1.

Pfam; PR0125; Stap_Strp_tox C; 1.

Pfam; PR0127; STAPH STREP_TOXIN.1; 1.

PROSITE; PR00277; STAPH STREP_TOXIN.1; 1.
                                                                                                                                                                                                                                                              140
                                                                                                                                                                                                                                                                                         61 SCPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNH 120
                                                                                                                                                                                                                                                                                                                                                                  200
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                                                                                                                                                                                     1 GLTISQEVFAQQDPDFSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHDLIYNV
                                                                                                                                                                                                                                                                                                                                                                     LEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETG
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                                                                                                                                                                                                                                                              SGPNYDKLKTELKNOEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNH
                                                                                                                                                          21 GLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNV
                                                                                                      Gaps
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                                                      Length 222;
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                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 YIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSNTS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222
25759 MW; 48BB7ADDCD91FBA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220 AA; 25600 MW; 92DB096E57906DF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 YIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSNTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            079AQ0;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                Ouery Match 88.7%; Score 1173; DB 2; Best Local Similarity 99.5%; Pred. No. 1.1e-79; Matches 221; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.7%; Score 1159; DB 2;
99.5%; Pred. No. 1.2e-78;
iive 0; Mismatches 1;
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type A exotoxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=MGAS500;
MEDLINE=92044323; PubMed=1940804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 219; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220
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220
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68 9

Gaps

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61 DQLLSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 IYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 IYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KKAVPFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 KKMVPFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 LYTNGPSKYETGYIKFIPKONKESFWFDFFPEPFFTQSKYLMIYKDNETLDSNTSQI 244
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"Characterization and clonal distribution of four alleles of in gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.;

L J. Exp. Med. 174:1271-1274 (1991).

E EMBL; X61561; CAA43760.1;

R EMBL; X61563; CAA43769.1;

R EMBL; X61564; CAA43763.1;

R EMBL; X61565; CAA43765.1;

R EMBL; X61565; CAA43765.1;

R EMBL; X61565; CAA43765.1;

R HSRP; A60108; A60108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=MGAS156, MGAS250, MGAS285, MGAS480, MGAS492,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                 1 1 22 Potential.
23 >236 type A exotoxin.
236 236 WW, 29DF2AD575623A84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1239; DB 2;
Pred. No. 1.4e-84;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 236 AA
                                                                                                                                               PRINTS; PRO0279; BACTRLTOXIN.
PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
Signal.
NON TER 1 1 22 Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO, GO:0005576; C:extracellular; IEA.
GO, GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact endotox.
InterPro; IPR006177; Bctr tox.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006126; Staph/Strept_tox.
       InterPro; IPR006126; Staph/Strept_tox.
InterPro; IPR006173; Staph_tox_OB.
Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF02876; Stap_Strp_tox_C; 1.
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Name=speA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92044323; PubMed=1940804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.2<sup>3</sup>
Matches 234; Conservative
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NON TER
SEQUENCE
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Q57453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DQLLSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVBYYHLCYLCENABRSAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 DQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSAC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 IYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KKAVPFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 KKMVFFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 LYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSNTSQI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 LYTNGPSKYETGYIKFIPKOKESFWFDFFPEPEFTQSKYLMIYKDNETLDSNTSQ1 236
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STRAIN=MGAS485, MGAS491, MGAS495, and MGAS624;

K MEDLINE=92044323, PubMed=1940804,

K MEDLINE=92044323, PubMed=1940804,

Nelson K., Schlievert P.M., Selander R.K., Musser J.M.,

R Characterization and clonal distribution of four alleles of the gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.";

L J. Exp. Med. 174:1271-1274(1991).

R EMBL; X61569; CAA43766.1;

R EMBL; X61571; CAA43766.1;

R EMBL; X61571; CAA43768.1;

R EMBL; X61571; CAA43769.1;

R EMBL; X61571; CAA43709.1;

R PIR; A60108; A60108.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <1 22 Potential.
23 >236 type A exotoxin.
236 236 AA; 27454 MW; 3FB3F41ABDC13A84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q54779; Q54613; Q54736; Q54740; Q54741;

1. NOV-1996 (TrEMBLrel. 01, Created)

01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.8%; Score 1240; DB 2;
99.6%; Pred. No. 1.2e-84;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potential.
type A exotoxin.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR006992; Bact endotox.
InterPro; IPR006173; Bact tox.
InterPro; IPR006123; Stap/Strept toxi.
InterPro; IPR006125; Stap/Strept tox.
InterPro; IPR006125; Stap/Strept tox.
InterPro; IPR006133; Staph.tox.08.
Pfam; PF01123; Stap Strp toxin; 1.
Pfam; PF012876; Stap Strp toxin; 1.
PROSTIE; PS00279; BACTRITOXIN.
PROSTIE; PS00277; STAPH_STREP_TOXIN 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 AA
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InterPro; IPR006177; BctrI tox.
InterPro; IPR006123; Stap/Strep_toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005576; C:extracellular; IEA. GO; GO:0009405; P:pathogenesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Type A exotoxin precursor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 99.6
Matches 235, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pyogenes.
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NCBI_TaxID=1314;
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NCBI_TaxID=1314;
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Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
Hayashi H., Hattori M., Hamada S.;
"Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
large-scale genomic rearrangement in invasive strains and new insights
into phage evolution."
Genome Res. 13:1042-1055(203).
EMBL; AR014161; AAM79908-1; -.
EMBL; AP005142; BAC63655.1; -.
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STATAL=MGAS115 / Serotype M3;
MEDLINE=22131808; bubMed=12122206; DOI=10.1073/pnas.152298499;
MEDLINE=22131808; bubMed=12122206; DOI=10.1073/pnas.152298499;
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D., Campbell D.S., Smith T.M., McOrmick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.;
"Genome sequence of a serotype M3 strain of group A Streptococcus: phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                       Query Match 99.5%; Score 1315; DB 1; Length 251; Best Local Similarity 99.6%; Pred. No. 3.3e-90; Matches 250; Conservative 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pyogenes (serotype M3).
Bacteria: Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                              29246 MW; 54001FE4CCCBFCC3 CRC64;
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01-007-2002 (TrEMBLrel. 22, Last sequence update)
01-007-2004 (TrEMBLrel. 28, Last annotation update)
Exotoxin type 4-phage associated (SpeA precursor).
Name=speA3; OrderedLocusNames=SP80560, SpyM3_1301;
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Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002)
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251 AA;
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NCBI_TaxID=198466;
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X MEDLINE=92044323; PubMed=1940804;
A Nelban K., Schlidevert P.M., Schladevert P.M., Sch
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
05-JUL-2004 (TrEMBLrel. 77, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1314; DB 2;
Pred. No. 3.9e-90;
1; Mismatches 1;
HESP; POLSES; 1SEB.

GO; GO:0009576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact endotox.
InterPro; IPR006177; Bctrl tox.
InterPro; IPR006173; Stap/Strept toxin.
InterPro; IPR006126; Staph/Strept toxin.
InterPro; IPR006126; Staph/Strept toxin.
InterPro; IPR006173; Staph tox 0B.
Ffam; PF01123; Stap Strp toxin; I.
Ffam; PF02175; Staph Strp toxin; I.
Fram; PF02175; Staph Strp toxin; I.
FRNTS; PR00279; BACTRLTOXIN.
PROSITE; PS00277; STAPH STREP TOXIN 1; I.
PROSITE; PS00278; STAPH STREP TOXIN 1; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I -> L (in Ref. 2).
TNKKOMVTAQELDYK -> QIKNGNCSRISYT (in Ref.
                                MISCELLANBOUS: This toxin seems to be coded by bacteriophage T12 SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
SUBUNIT: Binds to major histocompatibility complex class II beta
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SQEVPAQODDD -> LPKGICSTRPK (in Ref. H -> Q (in Ref. 2).
S -> N (in Ref. 2).
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InterPro; 1PR00617; Bctll tox.
InterPro; 1PR006123; Stap/Strep_toxin.
InterPro; 1PR006126; Staph/Strept tox.
InterPro; 1PR006126; Staph/Strept tox.
InterPro; 1PR006173; Staph_tox_OB_Pfam, PP01276; Stap_Strp_toxin.
Pfam; PP0123; Stap_Strp_toxin; 1.
PR011E3; PR00279; BACTRLTOXIN.
PROSITE; PS00279; STAPH STREP_TOXIN_1; 1.
PROSITE; PS00279; STAPH STREP_TOXIN_1; 1.
3D-structure; Signal; Toxin.
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1FNU; X-ray; -.
1FNV; X-ray; -.
1FNW; X-ray; -.
1HAA5; X-ray; -.
1LOX; X-ray; -.
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PUNCTION: Causative agent of the symptoms associated with scarlet
fever, have been associated with streptococcal toxic shock-like
disease and may play a role in the early events of rheumatic
                                                                                                                                                                                                                                                                                                                ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVR
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01-AUG-1988 (Rel. 08, Created)
01-ANG-1990 (Rel. 13, Last sequence update)
01-ANG-1900 (Rel. 145, Last annotation update)
Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=86166804; PubMed=3514452;
Weeks C.R., Ferretti J.J.;
"Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).
MEDLINE=99094887; PubMed=9878045; DOI=10.1093/emboj/18.1.9;
Papageorgiou A.C., Collins C.M., Gutman D.M., Kline J.B.,
O'Brien S.M., Tranter H.S., Acharya K.R.;
"Structural basis for the recognition of superantigen streptococcal pyrogenic exotoxin A (SpeAl) by MHC class II molecules and T-cell
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Johnson L.P., L'Italien J.J., Schlievert P.M.;
"Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is
related to Staphylococcus aureus enterotoxin B.";
Mol. Gen. Genet. 203:354-356(1986).
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                                                                                                   Query Match 99.5%; Score 1315; DB 1; Length 251; Best Local Similarity 99.6%; Pred. No. 3.3e-90; Matches 250; Conservative 0; Mismatches 1; Indels (
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                  By similarity.
Exotoxin type A.
By similarity.
; 54001FE4CCCBFCC3 CRC64;
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ALIGNMENTS

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C;Accession: H89668
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-558 «KUR»
A,Cross-references: UNIPROT:09EZM4; GB:BA000018; PID:g13701618; PIDN:BAB42911.1; GSPDB:
A,Experimental source: strain N315
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C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                         10 KMVFFVLVTFLGLTI-----SQEVFAQODPDPSQLHRSSLVKNLQNIYFLYEGD
                              38; Gaps
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     34.1%; Pred. No. 1.2e-17; rative 52; Mismatches 86; Indels
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A;Molecule type: DNA
A;Residues: 1-260 «KUR»
A;Cross-references: UNIPROT:099SU3; GB:BA000018; PID:g13701743; PIDN:BAB43036.1; GSPDB:0
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GB:BA000018; PID:g13701619; PIDN:BAB42912.1; GSPDB:
                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Staphylococcus aureus
C;Bete: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Bete: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: A9969
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shibb, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: C89884
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 RSACIYGGVTNHEGNHL-----EIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYK 178
179 VRKYLTDNKQLYTNGPSKYETGYIKFIPROKESFWFDFFPE--PEFTQSKYLMIYKDNET 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146 A;Accession: C89984 A;Status: preliminary
                                                                                   KAVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKF -- IPKNKESFWFDFFPEPEFTQS 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146 A;Accession: A89969 A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KKTCMYGGVTEHDGNQIDKNNSTDNSHNILIKVYENERNSLSFDIPTNKKNITAQEIDYK
                                                                                                                                                                                                                                                                                                                                                                                           enterotoxin YENT2 [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.5%; Score 337; DB 2; Length 136; 49.6%; Pred. No. 4.4e-18; ive 22; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enterotoxin P [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
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                                                                                                                                                                                             226 KYLMIYKDNETLDSNTSQIEVYLTT 250
                                                                                                                                                                                                                             38 OYLQIYNDNKTIDSSDYHIDVYLFT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Cross-references: UNIPROT:099T49;
A.Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::| : :||:|| |
122 VESKSINVEVHLTKK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 LDSNTSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 49.63
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: sep
C,Superfamily: enterotoxin B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-136 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
                                                                                      168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: yent2
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                       C,Accession: A3353
R;Bayles, K.W.; Iandolo, J.J.
J; Barteriol. 171, 4799-4806, 1989
A;Title: Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin
A;Reference number: A33953; MUID:89359112; PMID:2549000
A;Accession: A33953
A;Accession: A33953
A;Accession: A33953
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-258 cBAY.
A;Residues: 1-258 cBAY.
A;Cross-references: UNIPROY:P20723; GB:M28521; NID:g1492109; PIDN:AAB06195.1; PID:g75869
C;Superfamily: enterotoxin B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUD:21311952; PMID:11418146
A;Accession: E89969
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-260 cKUR>
A;Kesidues: 1-260 cKUR>
A;Cross-references: UNIPROT:Q99746; GB:BA000018; PID:g13701623; PIDN:BAB42916.1; GSPDB:GA:Experimental source: strain N315
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K.;
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R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DPVTHENVKSV----DQLRSHDLIYN----VSG--PNYDKLKTELKNQEMATLFKDKNVD 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 IYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNK 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQ-SLSFD-IETNKKMVTA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QELDYKVRKYLTDNKQLYTNGP--SKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMI 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 LKKM-VFFVLVTFLGLTISQ-EVFAQODPD---PSQLHR-----SSLVKNLQNIYFLYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DPVTHENVKSVDQLRSHDLIYN---VSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MENNKKYLKKMYFFVLVTFLGLTISQEVFA-QQDPDPSQLHRSSLVK--NLQNIYFLYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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36.2%; Pred. No. 8.4e-18;
Live 42; Mismatches 107; Indels 20;
                                                                                                                                                                                                                                                                                                                                                                                                                        20;
                                                                                                                                                                                                                                                                                                                                                            Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enterotoxin SeO [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                            ; Score 340; DB 2; Length 25; Pred. No. 5.9e-18; 47; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ||:|| : |::|| | xSDNKTLSTEHLHIDIYLYEK 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 YKDNETLDSNTSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                            25.7%;
ilarity 35.2%;
Conservative 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 36.2%
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C,Genetics:
A,Gene: seo
C,Superfamily: enterotoxin B
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 92; Conserv
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extracellular enterotoxin type G precursor [imported] - Staphylococcus aureus (strain N C)Species: Staphylococcus aureus
C)Species: Staphylococcus aureus
C)Species: Staphylococcus
C)Accession: G89968
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu
R, Kuroda, M.; Ohta, T.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
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                                                                                                                                                       69 DKFLAHDLIYNISDKKLKNYDKVKTELLNEGLAKKYKDEVVDVYGSNYYVNCYFSSKDNV 128
                                                                                                                                                                                                                                                       189 KARNFLINKKNLYEFNSSPYETGYIKFIENNGNIFWYDMMPAPGDKFDQSKYLMMYNDNK 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: 689958
A;Actus: preliminary
A;Molecule type: DNA
A;Redadues: 1-258 «KUR»
A;Coss-references: UNIPROT:085382; GB:BA000018; PID:g13701617; PIDN:BAB42910.:A;Experimental source: strain N315
                                                                                                                                                                                                                         124 ER----SACIYGGVTNHEGNHLEIP--KKIVVKVSIDGIQSLSFDIETNKKMVTAQELDY 177
                                                                                                                                                                                                                                                                                                                     178 KVRKYLTDNKOLYTNGPSKYETGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNE 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 DYKARHWLIKEKKLYEPDGSAFESGYIKFIEKNNISFWFDLFPKKELVPFVPYKFLNIYG 239
                                                                                                                           DQLRSHDLIYNVSG---PNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC--ENA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPE---FTQSKYLMIYK 232
                                                             62 HENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCE
                                MVF-PVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAE-----RSACIYGGVŢNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVŢAQEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 LKCMVFFVLVTFLGLTISQEVFAQQDPDP--SQLHRSSLVKN----LQNIYFLYEGDPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
36.4%; Score 481; DB 2;
Best Local Similarity 40.7%; Pred. No. 2.3e-28;
Matches 105; Conservative 46; Mismatches 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enterotoxin D precursor - Staphylococcus aureus C; Species: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNETLDSNTSQIEVYLTT 250
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DNKVVDSKSIKMEVFLNT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                            |:|| : :|||:|||
249 TVDSKSVKIEVHLTTK 264
                                                                                                                                                                                                                                                                                                                                                                                                                   TLDSNTSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Gene: seg
C.Superfamily: enterotoxin B
                                                                                                                           69
                                                                                                                                                                                                                                                                                                                                                                                                                 236
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C;Species: Staphylococcus
C;Accession: S06356, A01016
R;Bohach, G.A.; Schlievert, P.M.
Mol. Gen. Genet. 209, 15.20, 1987
A;Title: Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness the scension: S06356, MUID:88038352; PMID:2823067
A;Title: Nucleotide sequence of the staphylococcal enterotoxin C1
A;Residues: 1-266 <BOH>
A;Cross: UNIPROT:P01553; EMBL:X05815; NID:946566; PIDN:CAA29260.1; PID:946567
A;Cross: Cference: UNIPROT:P01553; EMBL:X05815; NID:946566; PIDN:CAA29260.1; PID:946567
A;Cross: Cference: UNIPROT:P015313377; PMID:6189824
A;Accession: A01816
A;Molecule type: protein
A;Residues: 28-75, IL',78-176, 'N',178-266 <SCH>
C;Genetics: enterotoxin B
C;Keywords: enterotoxin B
C;Keywords: enterotoxin
F;1-27/Domain: signal sequence #status predicted <SIG>F;120-137/Disulfide bonds: #status experimental <MAT>F;120-137/Disulfide bonds: #status experimental
                                                                               다
                                                      A;Title: Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests 1
A;Reference number: A33866; MUID:89327174; PMID:2473979
A;Accession: A33866
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-266 <COU>
A;Cross-references: GB:M28364; NID:g153003; PIDN:AAA26624.1; PID:g153004
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DQLRSHDLIYNVSG---PNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC--ENA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 ER----SACIYGGVTNHEGNHLEIP--KKIVVKVSIDGIQSLSFDIETNKKMVTAQELDY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKVTGGKTCMYGGITKHEGNHFDNGNLQNVLIRVYENKRNTISFEVQTDKKSVTAQELDI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KVRKYLTDUKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNE 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 MVF-FVLVTFLGLTISQEVFAQQDPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                   41.5%; Score 549; DB 2; Length 266; 44.1%; Pred. No. 2.3e-33; Live 52; Mismatches 73; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 41.5%; Score 540; DB 1; Length 266; Best Local Similarity 44.5%; Pred. No. 2.7e-33; Matches 114; Conservative 51; Mismatches 73; Indels 1
                                                                                                                                                                                                                                                                                                              F:1-27/Domain: signal sequence #status predicted <SIG> F:28-266/Product: enterotoxin C-2 #status predicted <MAT>
A;Residues: 28-66 <BOH2>
R;Couch, J.L.; Betley, M.J.
J. Bacteriol. 171, 4507-4510, 1989
A;Title: Nucleotide sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLDSNTSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:|| ::|||:|||
TVDSKSVKIEVHLTTK 264
                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 44.18
                                                                                                                                                                                                                                                            A;Gene: entC2
C;Superfamily: enterotoxin B
F;1-27/Domain: signal sequenc
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Matches
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C;Species: Staphylococcus aureus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: 811885
C;Accession: 811885
R;Hovde, C.J.; Hackett, S.P.; Bohach, G.A.
Mol. Gen. Genet. 220, 329-333, 1990
A;Title: Nuclectide sequence of the staphylococcal enterotoxin C3 gene: sequence compari
A;Reference number: 811885; MUID:90220508; PMID:2325627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A60114

Activation of the precursor of the process 
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A;Residues: 1-266 AHOV.
A;Cross-references: UNIPROT:P23313; GB:X51661; NID:946570; PIDN:CAA35972.1; PID:946571
C;Superfamily: enterotoxin B
----ERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKXMVTAQELDYK 178
                                               71 LRSHDLIYNVSG---PNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC--ENAER 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 ----SACIYGGVTNHEGNHLEIP--KKIVVKVSIDGIQSLSFDIETNKKAVTAQELDYKV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 VTGGKTCMYGGITKHEGNHFDNGNLQNVLVRVYENKRNTISFEVQTDKKSVTAQELDIKA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 RKYLTDNKOLYTNGPSKYETGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNETL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 VLVTFLGLTIS-QEVFAQQDPD--PSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVDQ
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A;Cross-references: UNIPROT:P34071
                                                                                                                                                                                                                                                                                                                                                                                                             :|| :|||||||
VDSKDVKIEVYLTTK 264
                                                                                                                                                                                                                                                                                                                                                         LDSNTSQIEVYLTTK 251
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|DSKSVKIEVHLTTK 264
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A,Molecule type: protein
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A; Molecule type: protein
A; Recession: A92065
A; Molecule type: protein
A; Recession: A92065
A; Molecule type: protein
A; Residues: 28-55, NND, 59-68, NE', 71, 'FDLIYL', 78-117,119-127, N', 129, 'D', 131-132, 'ENT', A; Respectioneral source: strain S-6
B; Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3311-3517, 1970
A; Title: The primary structure of staphylococcal enterotoxin B. II. Isolation, compositi A; Reference number: A22064; MUID:71007901; PMID:5470820
A; Contents: annotation; chymotryptic peptides
B; Huang I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3493-3510, 1970
A; Title: The primary structure of staphylococcal enterotoxin B. I. Isolation, compositic A; Reference number: A22063; MUID:71007900; PMID:5470819
A; Contents: annotation; tryptic peptides
B; Schantz, B.J.; Roessler, W.G.; Wagman, J.; Spero, L.; Dunnery, D.A.; Bergdoll, M.S.
Biochemistry 4, 1011-1016, 1965
A; Contents: annotation of staphylococcal enterotoxin B.
A; Reference number: A00548; MUID:6035792, PMID:4953912
A; Contents: annotation; biological source of protein
B; Contents: annotation; biological source of protein
B; A; Reference number: 309, 823-828; 1992
A; Title: Identification of functionally active fragments of staphylococcal enterotoxin B
A; Reference number: S27240; MUID:93049338; PMID:1425690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 24-Apr-1984 #sequence revision 15-Oct-1996 #text_change 09-Jul-2004
C;Date: 24-Apr-1984 #sequence revision 15-Oct-1996 #text_change 09-Jul-2004
C;Datesion: S27360; A2065; $\overline{S}$ \overline{Z}$ \overlin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 VLVTFLGLTIS-QEVFA--QOPPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVDQ
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A; Residues: 28-42;188-148

C; Superfamily: enterotoxin B

C; Keywords: enterotoxin, extracellular protein; toxin

F; 1-27/Domain: signal sequence #status predicted <SIG>

F; 28-26/Product: enterotoxin B #status experimental <MAT>

F; 120-140/Disulfide bonds: #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enterotoxin B precursor - Staphylococcus aureus
                                                                                                                                                                                                                                                                              240 TSQIEVYLTTK 250
                                                                                                                                                                                                                              241 TSQIEVYLTTK 251
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Best Local Similarity
Matches 123; Conserv
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C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004
C;Accession: $18789
E;Nelson: K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A;Title: Characterization and clonal distribution of four alleles of the speA gene enco A;Reference number: $18782; MUID: 92044323; PMID: 1940804
A;Accession: $18789
A;Accession: $18789
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEL>
A;Residues: 1-236 <NELS
A;Rocross-references: UNIPROT: 054696; EMBL: X61573; NID: 947303; PIDN: CAA43771..1; PID: 94730.
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: A26152
R;Johnson, L.P.; L'Italian, J.J.; Schlievert, P.M.
Mol. Gen. Genet. 203, 354-356, 1986
A;Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to Sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DQLRSHDL1YNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSAC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 IYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENAERSACLYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIEQIKN-GNCSRISYTVR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Streptococcus sp.
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DQLLSHDLIYNVSGLNYDKLKTELKNREMSTLFKNKNVDIYGVEYYYHCYLCRNAKRRAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 IYGGVTNHEGNHLEIPKNILVKVSIDGIQSLSFDIETSKKMYTAQELDYKVRKHLTDNKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KKIVYFVLAIFLGLTTSQEVFAQODPNPSQLHRSSLVKNLQNIYFLYEGDPVVHENVKSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 KKMVPFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MENNIKKVLKKMVFFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           streptococcal pyrogenic exotoxin type A precursor - Streptococcus sp. N;Alternate names: scarlet fever toxin; SPE type A (speA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: enterotoxin B
C;Keywords: exotoxin
F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F;23-236/Product: exotoxin A (fragment) #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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9.1e-75;
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83.7%; Pred. No. 2.9e-72;
cive 7; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.9%; Score 1109; D
88.6%; Pred. No. 9.1e
ive 14; Mismatches
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C;Superfamily: enterotoxin B
C;Keywords: exotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 88.6
Matches 209; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 210; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: speA
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                                                                                                              A. Accession: S18788

A. Accession: S18788

A. Accession: S1878

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A. Accession: S1878

A. Accession: S1878

A. Recession: S1878

A. Recession: S1878

A. Recession: S1878

A. Recession: S1878

A. Cross-references: EMBL. X61563; NID: 947301; PIDN: CAA43761.1; PID: 947302

A. Recession: S1879

A. Cross-references: EMBL. X61563; NID: 947301; PIDN: CAA43761.1; PID: 947302

A. Accession: S1879

A. Accession: S1879

A. Recession: S1879

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A. Accession: S18
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                               A;Cross-references: EMBL:X61562; NID:g47299; PIDN:CAA43760.1; PID:g47300
A;Experimental source: strain MGAS251 isolate California unassignd phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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C,Superfamily: enterotoxin B
C;Reywords: exotoxin
F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>F;23-236/Product: exotoxin type A (fragment) #status predicted <MAT>
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A; Experimental source: Streptococcus pyogenes strain MGAS493 isolate France unassigned FA; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A; Ascassion: 318797
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 9-244 < MBH-
A; Residues: 9-244 < MBH-
A; Resperimental source: Streptococcus pyogenes strain MGAS494 isolate France unassigned p
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A; Molecule type: DNA
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 9-228 < MES>
A; Cross-references: EMBL: X61554; NID: 947327; PIDN: CAA43752.1; PID: 947328
A; Cross-references: EMBL: X61554; NID: 947327; PIDN: CAA43752.1; PID: 947328
A; Cross-references: EMBL: X61554; NID: 947327; PIDN: CAA43752.1; PID: 947328
A; Residues: 9-228 < MES>
A; Residues: speak; speak
C; Superfamily: enterotoxin B
C; Superfamily: enterotoxin B
C; Superfamily: enterotoxin B
C; Superfamily: exterotoxin Extatus predicted < SIG>
F; 1-30/Domain: signal sequence #status predicted < MAT>
F; 1-31/Product: exotoxin type A #status predicted < MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    excloxin type A precursor (allele 3) - Streptococcus pyogenes phage (strain MGASI58 isol NAlternate names: scarlet fever toxin (species: Streptococcus pyogenes phage A; Variety: strain MGASI58 isolate bhage A; Variety: strain MGASI58 isolate Nebraska; strain MGASI58 isolate Yugoslavia; strain MGASI58 isolate Nebraska; strain MGASI58 isolate Variety: strain MGASI58 isolate Nebraska; strain MGASI58 isolate Sequence revision 29-dan-1993 #text_change 16-Jul-1999 (spacession: S18783; S18794; S18801; S18798 #text_change 16-Jul-1999 R; Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A; Fitle: Characterization and clonal distribution of four alleles of the speA gene encod A; Reference number: S18782; MUD:92044323; PMID:1940804
A; Accession: S18783
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Experimental source: strain MGASI58 isolate Nebraska unassigned phage
A; Moces: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A; Accession: S18793
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Molecule 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THENVKSVDQLLSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVSYYHLCYLC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMYTAQELDYKVR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKAVTAQELDYKVR 180
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A;Cross-references: EMBL:X61569; NID:g47313; PIDN:CAA43767.1; PID:g47314
A;Experimental source: strain MGAS485 isolate Yugoslavia unassigned phage
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TSQIEVYLTTK 251
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exotoxin type A precursor (allele 2) - Streptococcus pyogenes phage (strain MGAS250 iso)
NyAlternate names: scarlet fever toxin
NyAlternate names: scarlet fever toxin
Syspecies Streptococcus pyogenes phage
A;Variety: strain MGAS250 isolate California; strain MGAS251 isolate California; strain
Solate United Kingdom; strain MGAS496 isolate Germany
C;Date: 29-Jan-1993 #sequence travision 29-Jan-1993 #text change 16-Jul-1999
C;Accession: S18786; S18787; S18789; S18790; S18795; S18799;
R;Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
A;Title: Characterization and clonal distribution of four alleles of the speA gene enco-A;Reference number: S18782; MUID:92044323; PMID:1940804
                                                                                                                                  Appleatus: Marter acts acquerce not shown, translation not shown.

A, Residues: 1-236 <NBZ>
A, Rocestues: strain MGAS491 isolate United Kingdom unassigned phage
A, Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A, Residues: 1-236 <NBZ>
A, Residues: 1-236 <NBZ
A, Residues: 1-236
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A;Cross-references: EMBL:X61561; NID:g47297; PIDN:CAA43759.1; PID:g47298
A;Experimental source: strain MGAS250 isolate California unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-216 <NEO>
A;Cross-references: EMBL:X61571; NID:g47323; PIDN:CAA43769.1; PID:g47324
A;Experimental source: strain MGAS495 isolate Germany unassigned phage
A;Noce: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
the nucleotide sequence was submitted to the EMBL Data Library, September 1991
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;Reywords: exotoxin
;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
;23-236/Product: exotoxin type A (fragment) #status predicted <MAT>
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
                                                                                                   shown; translation not shown
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1; Mismatches 1
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                                                         A;Accession: S18794
A;Status: nucleic acid sequence not
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Best Local Similarity 99.2<sup>3</sup>
Matches 234; Conservative
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

September 17, 2005, 01:00:14; Search time 18.153 Seconds (without alignments) 1330.382 Million cell updates/sec Run on:

US-10-002-784A-16 1322 1 MENNKKVLKKMVFFVLVTFL......KDNETLDSNTSQIEVYLTTK 251 Perfect score: Sequence:

283416 seqs, 96216763 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	exotoxin type A pr	V	exotoxin type A pr	ecn	streptococcal pyro	enterotoxin B prec	enterotoxin C3 - S	enterotoxin C-2 pr	enterotoxin C-1 pr	extracellular ente	enterotoxin D prec	enterotoxin SeO [i	ΧE	enterotoxin P [imp	enterotoxin SeN [i	enterotoxin E prec	enterotoxin A prec	extracellular ente	enterotoxin SEM [i	extracellular ente	exotoxin C precurs	enterotoxin Yent1	exotoxin 11 [impor	hypothetical prote	exotoxin 15 [impor	exotoxin 13 (impor	exotoxin 10 [impor	¥	exotoxin 9 [import
SUMMAKIES	ID	829659	S18783	S18786	S18789	A26152	ENSAB6	S11885	A60114	ENSAC1	G89968	A33953	E89969	A89969	C89984	Н89968	A28179	A28664	G89991	D89969	C89969	A30509	B89969	D89807	A89942	C89808	F89807	C89807	B89992	B89807
	DB	-	0	~	~	н		~	7		~	~	0	~	7	~	~	7	~	~	7	7	0	0	7	0	~	7	N	7
	Length	251	236	236	236	250	266	266	266	266	258	258	260	136	260	258	257	257	240	239	242	235	133	231	157	227	232	234	234	292
d	Query Match	99.5	93.7	93.3	83.9		43.6	41.7	41.5	41.5	36.4	25.7	25.6	25.5	25.4	23.6		23.2	23.1	20.0	19.0	٠	13.2	9.6	9.7	9.5	9.8	9.8	8.4	8.4
	Score	1315	1239	1234	1109	1075.5	576.5	551.5	549	548	481	340	338	337	336	311.5	308	307	305.5	264	251.5	211	174	129.5	128	125	114	114	111	111
	Result No.	-	7	m	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote toxic shock syndro exotoxin 7 [import FUSION, methionine ORF MSV181 hypothe hypothetical prote transport protein desmocollin 1b pre desmocollin 1a pre DSC1a precursor - DSC1b precursor - DSC1b precursor - hypothetical prote immunoglobulin A1 hypothetical prote	prrC protein - Esc probable membrane
H82885 XCSASI H89806 H89806 T28342 G50604 G50604 A48910 A48910 137281 137281 13728 C55008	S09627 C97252
0 + 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0
825 231 231 231 434 434 1790 7790 1790 1790 1367 1856 1856	396 235
88888888777777 	7.8
109.5 108.5 108.5 108.5 108.5 105.5 105.1 105.1 105.5 104.5	103.5
0 11 12 13 13 13 13 13 13 13 13 13 13 13 13 13	4 4 5

ALIGNMENTS

RESULT 1

S29659	
exotoxin type A prec	exotoxin type A precursor (allele 1) - Streptococcus pyogenes phage T12
N;Alternate names: e	N;Alternate names: erythrogenic toxin; scarlet fever toxin
C;Species: Streptoco	C;Species: Streptococcus pyogenes phage T12
C;Date: 10-Sep-1999	C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 10-Sep-1999
C; Accession: S29659;	C;Accession: S29659; S18782; S18784; S18785; S18791; S18 ⁷ 96; S18797; S18800
R; Weeks, C.R.; Ferretti, J.J.	tti, J.J.
Infect. Immun. 52, 144-150, 1986	44-150, 1986
A; Title: Nucleotide	A, Title: Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin)
A; Reference number:	A; Reference number: 829659; MUID:86166804; PMID:3514452
A; Accession: S29659	
A, Molecule type: DNA	
A, Residues: 1-251 <wee></wee>	88>
A; Cross-references:	A; Cross-references: GB: U40453; EMBL: M19350; NID: g1877426; PIDN: AAC48868.1; PID: g1877430
R;Nelson, K.; Schlie	R; Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
100 T 100 TECT TET TOTAL TITLE TO	1001

J. Exp. Med. 174, 1271-1274, 1991
A;Title: Characterization and clonal distribution of four alleles of the speA gene encor A;Areference number: S18782; MVID:92044323; PMID:1940804
A;Accession: S18782
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

A;Residues: 9-244 <NEL>
A;Cross-references: EMBL:X61560; NID:g47287; PIDN:CAA43758.1; PID:g47288
A;Experimental source: Streptococcus pyogenes strain MGA5156 isolate Nebraska unassigne.
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991

A.Accession: 518784
A.Status: nucleic acid sequence not shown; translation not shown
A.Status: nucleic acid sequence not shown; translation not shown
A.Status: nucleic acid sequence not shown; translation not shown
A.Rossiques: 9-244 <nEA.
A.Stxperimental source: Streppcococus pyogenes strain MGAS165 isolate Minnesota unassign.
A.Stxperimental source: Streppcococus pyogenes strain MGAS165 isolate Minnesota unassign.
A.Accession: S18785
A.Accession: S18785
A.Accession: cacid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 9-244 <NEZ>

A;Cross-references: EMBL:X61559; NID:g47293; PIDN:CAA43757.1; PID:g47294 A;Experimental source: Streptococcus pyogenes strain MGAS167 isolate Texas unassigned pi A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991 A;Accession: S18791 A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA

A, Residues: 9-244 <NEY>
A, Residues: 9-244 <NEY>
A, Cross-references: EMEL:X61555, NID:947309; PIDN:CAA43753.1; PID:947310
A, Experimental source: Streptococcus pyogenes strain MGA5327 isolate Arizona unassigned A, Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991

A;Accession: S18796
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule s: 9-244 <NEO>
A;Residues: 9-244 <NEO>
A;Cross-references: EMBL:X61557; NID:g47319; PIDN:CAA43755.1; PID:g47320

250 VDSKDVKIEVYLTTK 264

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RESULT 15

US-09-751-708A-10

Sequence 10, Application US/09751708A

Sequence 10, Application Wolf-09-51708A

Sequence 10, Application Wolf-09-51708A

SEQUENCE 10, APPLICATION

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE

FILE REFERENCE: 751708

CURRENT APPLICATION NUMBER: US/09/751,708A

CURRENT PILING DATE: 1999-12-28

PRIOR FILING DATE: 1999-12-28

NUMBER OF SEQ ID NOS: 166

SOFTWARE: Patentin version 3.1

SEQ ID NO 10

LENGTH: 266

TYPE: PRT

CORGANISM: Staphylococcus aureus

US-09-751-708A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 TRHYLVKNKKLYEFNNSPYETGYIKFI-ENENSFWYDWMPAPGDKFDQSKYLMMYNDNKM 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 ----ERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYK 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 43.6%; Score 576.5; DB 10; Length 266; Best Local Similarity 48.2%; Pred. No. 1.3e-41; Matches 123; Conservative 38; Mismatches 75; Indels 19; Gaps
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250 VDSKDVKIEVYLTTK 264
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                                                                                                                                                                                                                        Gaps
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Sequence 2, Application VS.200302962A1
GENERAL INFORMATION:
GENERAL INFORMATION:
Elmsie, Robyn E.
Potter, Terence A.
TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Sulte 3500
                                                                                                                                           DB 17; Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 80203

COMPUTER READABLE FORM:
MEDIUM TERPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 29-Jan-2003
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                         Indels
                                                                                                                                                                           33;
                                                                                                                                                           Pred. No. 6.7e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-29-C1
                                                                                                                                         81.4%; Score 1075.5;
83.7%; Pred. No. 6.7e-
                                                                                                                                                                        7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/580,806
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 255 amino acids
                                                                                          ORGANISM: Streptococcus pyogenes
PRIOR FILING DATE: 2000-08-30
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
LENGTH: 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS
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STATE: Colorado
COUNTRY: U.S.A.
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Matches 210; Conservative
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Sequence 10, Application US/09870759;
Patent No. US20020177551A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION:
COMPOSITION NUMBER: US/09/870,759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT PILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
FIRST RELING DATE: 2000-05-30
WINDOW OF THE TOWN NUMBER: US/09/870,759
FIRST PILING DATE: 2000-05-30
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44.5%; Score 588; DB 15;
Best Local Similarity 47.2%; Pred. No. 1.2e-42;
Matches 119; Conservative 41; Mismatches 76;
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48.2%; Pred. No. 1.3e-41;
tive 38; Mismatches 75;
TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-354-948-2
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SOFTWARE: PatentIn version 3.1
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Matches 123; Conservative
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FILE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE; FILE REFERENCE: 38373-18918
FILE REFERENCE: 38373-18918
CURRENT APPLICATION NUMBER: US/10/428,817A
CURRENT FILING DATE: 2003-05-05
FRIOR APPLICATION NUMBER: US 60/378,988
FRIOR APPLICATION NUMBER: US 60/389,366
FRIOR APPLICATION NUMBER: US 60/406,697
FRIOR PILING DATE: 2002-06-15
FRIOR PELING DATE: 2002-08-29
FRIOR FILING DATE: 2002-08-29
FRIOR FILING DATE: 2002-00-01
FRIOR FILING DATE: 2002-10-01
FRIOR FILING DATE: 2002-10-01
FRIOR FILING DATE: 2003-10-02
FRIOR FILING DATE: 2003-10-03
FRIOR FILING DATE: 2003-01-09
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
TITLE REFERENCE: FILE REFERENCE 650884
CURRENT APPLICATION NUMBER: US/10/937,758A
CURRENT FILING DATE: 2004-09-08
PRIOR APPLICATION NUMBER: 09/650,884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 THENVKSVDQLLSHDLIXNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC 120
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                                                                                                                                                                        ; Sequence 16, Application US/10428817A; Publication No. US20040214783A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Streptococcus pyogenes
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Best Local Similarity 83.73
Matches 210; Conservative
                                           240 TSQIEVYLTTK 250
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            241 TSQIEVYLTTK 251
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US-10-937-758A-20
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US-09-751-708A-20
S-09-751-708A-20
S-09-751-708A-20
Publication No. US20030157113A1
GENERAL INFORMATION:
APPLICANT TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE;
FILE REFERENCE: 751708
CURRENT PILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 60/173,371
PRIOR APPLICATION NUMBER: 1999-12-28
NUMBER OF SEQ ID NOS: 166
NUMBER OF SEQ ID NOS: 166
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                                                                                                                                                                                        DB 9; Length 250;
                                                                                                                                                                                                                                        33; Indels
                                                                                                                                                                                        81.4%; Score 1075.5; DB
83.7%; Pred. No. 6.7e-85;
iive 7; Mismatches 33
                                                                                           ; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-870-759-20
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NUMBER OF SEQ ID NOS: 166
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
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SEQ ID NO 20
LENGTH: 250
                                                                                                                                                                                                              Best Local Similarity 83.7
Matches 210; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVR 180
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                                                                                                                                                                                                                                                                                                                                                                                                                          Length 251;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/231/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 26
LENGTH: 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 85.9%; Score 1136; DB 14; Best Local Similarity 98.2%; Pred. No. 3.2e-90; Matches 217; Conservative 1; Mismatches 1;
                                                      NAME: Skoog, Mark T
REGISTRATION NUMBER: 40,178
REFERENCE/DOCKET NUMBER: 600.346USWO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELERA: 612-332-9081
TELERA: cUnknown>
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
98.9%; Score 1308; DB 9;
Best Local Similarity 99.2%; Pred. No. 4.8e-105;
Matches 249; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
APPLICATION NUMBER: 60/032,930
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
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US-10-002-784A-26
Sequence 26, Application US/10002784A
Publication No. US20030036644A1
GENERAL INFORMATION:
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TSQIEVYLTTK 251
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APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
                                                                           ELKNOEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 150
                                                                                                  62 ELKNQEMATLFYDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
                                                                                                                                                                                                                 91 BLKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 150
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2 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIXNVSGPNYDKLKT
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TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT APPLICATION NUMBER: 08/882,431; 09/144,776
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
PRIOR RILING DATE: 97-06-25; 98-09-01
NUMBER OF SQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 85.9%; Score 1136; DB 14; Best Local Similarity 98.2%; Pred. No. 8.9e-90; Matches 217; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: mutant SpeA-mutant SpeB fusion US-10-002-784A-27
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US-10-002-784A-27
Sequence 27, Application US/10002784A
Publication No. US20030036644A1
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US-09-870-759-20
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                            APPLICANT: Roggiani, Manuela
APPLICANT: Stochr, Jennifer
APPLICANT: Stochr, Jennifer
APPLICANT: Obliguas
TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
FILE REPERENCE: 600.311USWO
CURRENT APPLICATION NUMBER: US/08/973,391A
CURRENT APPLICATION NUMBER: US/08/973,391A
RIOR APPLICATION NUMBER: PC7/US96/10252
PRIOR FILING DATE: 1996-06-07
PRIOR FILING DATE: 1996-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PALENTIN NOSE: 13
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Publication No. US20020086813A1
GENERAL INFORMATION:
APPLICANT: Regents of the University of Minnesota
TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A
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ZIP: 55402-0903

COMPUTER READABLE PORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/308,830
FILING DATE: 04-Aug-1999
CLASSIFFCATION: <URKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1308; DB 8;
Pred. No. 4.8e-105;
0; Mismatches 2;
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APPLICATION NUMBER: PCT/US97/22228
FILING DATE: 05-DEC-1997
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CORRESPONDENCE ADDRESS:
ADDRESSE: Merchant & Gould P.C.
STREET: P.O. Box 2903
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.9%;
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Best Local Similarity
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GENERAL INFORMATION:

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE

FILE REFERENCE: 38373-189118

CURRENT APPLICATION NUMBER: US 60/378,988

PRIOR APPLICATION NUMBER: US 60/378,988

PRIOR APPLICATION NUMBER: US 60/378,988

PRIOR PILING DATE: 2002-05-08

PRIOR APPLICATION NUMBER: US 60/406,697

PRIOR FILING DATE: 2002-06-15

PRIOR FILING DATE: 2002-06-28

PRIOR FILING DATE: 2002-06-28

PRIOR FILING DATE: 2002-10-01

PRIOR FILING DATE: 2002-10-01

PRIOR FILING DATE: 2002-10-02

PRIOR FILING DATE: 2002-10-02

PRIOR FILING DATE: 2003-10-02

PRIOR FILING DATE: 2003-10-02

PRIOR FILING DATE: 2003-10-03

PRIOR FILING DATE: 
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                                                         KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSN
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                                                                                                                                                                                                                                                                                                                                                                Sequence 163, Application US/10428817A Publication No. US20040214783A1 GENERAL INFORMATION:
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US-08-973-391A-13
US-08-973-391A-13
Sequence 13, Application US/08973391A
Publication No. US20020054887A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ; ORGANISM: Streptococcus pyogenes US-10-428-817A-163
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US-10-428-817A-163
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ADDRESSEE: Charles H. Harris
STREET: US Army MRMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent A
CITY: FORT DETRICK
THENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1322; DB 17;
Pred. No. 2.9e-106;
                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Bacterial Superantigen Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/882,431B
FILING DATE: June 25, 1997
ATTORNEY/AGENT INDEMATION:
NAME: Charles H. Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/10/767,687
FILING DATE: 29-Jan-2004
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Ur
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                             RESULT 3
US-10-767-687-16
Sequence 16, Application US/10767687
Publication No. US20050064526A1
GENERAL INFORMATION:
MARK A. Olson
Sina Bavari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (301) 619-2065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 251; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: MARYLAND
                                                                                                                                          TSQIEVYLTTK 251
                                                                                                                                                               241 TSQIEVYLTTK 251
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Best Local Similarity
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                                                                                                                                                                                                                                          DB 8; Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: streptococcal pyrogenic exotoxin-A mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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; Pred. No. 2.9e-106;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Bacterial Superantigen Vaccines FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR PILING DATE: 2001-11-26
PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 16
LENGTH: 251
                                                                                                                                                                                                                                        100.0%; Score 1322; DB 8;
100.0%; Pred. No. 2.9e-106;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/10002784A Publication No. US20030036644A1 GENERAL INFORMATION:
    TELECOMMUNICATION INFORMATION:
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Best Local Similarity 100.0%;
Matches 251; Conservative 0.
                    TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ulrich, Robert G.
                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.(
Matches 251; Conservative
                                                                                                                                          Unknown
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                                                                                                                   TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
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Gaps

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September 17, 2005, 00:44:58; Search time 77.8484 Seconds (without alignments) 1305.574 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MENNKKVLKKMVFFVLVTFL.....KDNETLDSNTSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. / cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

1. / cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

3. / cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3. / cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

3. / cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

3. / cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

3. / cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

3. / cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

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4. / cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

5. / cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

6. / cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

7. / cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

8. / cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

9. / cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1812044 seqs, 404927589 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1322
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                    Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 16, Appl	Sequence 16, Appl	Sequence 16, Appl	Sequence 163, App	Sequence 13, Appl	Sequence 13, Appl	Sequence 26, Appl	Sequence 27, Appl	Sequence 20, Appl	Sequence 20, Appl	Sequence 16, Appl
SUMMARIES		ΩI	US-08-882-431-16	US-10-002-784A-16	US-10-767-687-16	US-10-428-817A-163	US-08-973-391A-13	US-09-308-830-13	US-10-002-784A-26	US-10-002-784A-27	US-09-870-759-20	US-09-751-708A-20	US-10-428-817A-16
		DB	8	14	17	16	8	σ	14	14	σ	10	16
		Length	251	251	251	251	251	251	220	468	250	250	250
•	Query	Match Length DB	100.0	100.0	100.0	99.5	98.9	98.9	85.9	85.9	81.4	81.4	81.4
		Score	1322	1322	1322	1315	1308	1308	1136	1136	1075.5	1075.5	1075.5
	Result	No.	7	8	m	4	S	9	7	80	σ	10	11

20,		_	a	_	٠.	Sequence 12, Appl	Sequence 12, Appl		7		9	ä	ä	ω̈́	ω	.0,	14,	e 14	1	16	,	Sequence 12, Appl	Sequence 12, Appl	w	_	4	18	٦	æ	ശ	m	9	Sequence 2, Appli	
7 US-10-937	5 US-10-35	0	10 US-09-751-708A-10	y	US-1	9 US-09-150-947B-12	US-1	US-1	US-1	14 US-10-002-784A-6			17 US-10-767-687-10	US-10-002-784	17 US-10-767-687-8		8 US-08-882-431-14	US-10	17 US-10-767-687-14	6 US-10-428-817	-08	₽		16 US-10-428-817A-8		17 US-10-923-324-4			8 US-08-882-431-8	7	17 US-10-923-324-3	7	17 US-10-923-324-2	
250	255	266	566	266	266	239	239	566	238	266	566	239	239	566	266	239	566	566	266	566	265	566	266	266	266	240	239	240	265	240	240	240	240	
81.4	44.5	٠	43.6	43.6	43.6	43.6	43.6	43.5	43.4	42.9	42.9	42.6	42.6	•	42.2	•		41.8	41.8	41.7	41.5	41.5	41.5	41.5	41.5	41.4	41.2	41.1		40.5	40.5	•	40.2	
	288	576.5	576.5	576.5	576.5	576	576	575	574	567.5	567.5	563	563	558.5	558.5	558	553	553	553	551.5	549	548	548	548	548	547	545	544	542	536	535	533	532	
12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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Sequence 16, Application US/0882431

Sequence 16, Application US/0882431

Publication No. US20030009015A1

GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: John Moran
STREET: US Army MRMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
COMPUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/882,431
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/08/
FILLING DATE: June 25, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: MOTAIL, JOHN
REGISTRATION NUMBER: 26,313
REFERENCE/POCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
US-08-882-431-16
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Roggiani M, Stoehr J,
  (MINU ) UNIV MINNESOTA
            WPI; 1997-099936/09.
       Schlievert PM,
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Ohlendorf

Mutant SPE-A toxin with at least one amino acid change is substantially non-lethal - used in vaccine composition for treatment of cancer and streptococcal toxic shock syndrome etc.

Example 4; Page; 102pp; English.

The present sequence is a non-lethal Streptococcus pyogenes Streptococcal toxin A (SPE-A) mutant, which can be used to produce vaccines to protect animals against wild type SPE-A and to treat cancer and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fascitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A can be selectively toxic to T cell lymphoma cells. N.B. Sequence not given in the specification, but constructed using the wild type SPE-A sequence given on pages 77-79

Sequence 251 AA;

ö 61 THENVKSVDQLLSHLLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLS 120 THENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC 120 1 MENNKKVLKKOMVFFVLVTFLGLTISQEVFAQQDPDFSQLHRSSLVKNLQNIYFLYEGDFV 60 1 MENNKKVLKKMVFFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPV 60 0; Gaps Query Match 98.2%; Score 1298; DB 2; Length 251; Best Local Similarity 98.8%; Pred. No. 4.9e-109; Matches 248; Conservative 0; Mismatches 3; Indels (19 셤 ò

ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVR 180 121 8 ò ò

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TSQIEVYLTTK 251 241

241 TSQIEVYLTTK 251

Search completed: September 17, 2005, 01:09:41 Job time : 84.0376 secs

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ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMYTAQELDYKVR 180
toxin A (SPE-A) mutant, which can be used to produce vaccines to protect toxic shock syndrome (STS-A and to treat cancer and streptococcal toxic shock syndrome (STS). The mutant SPE-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fascitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A and be selectively toxic to T cell lymphoma cells. N.B. Sequence not given in the specification, but constructed using the wild type SPE-A sequence given on pages 77-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcal; toxin A, SPE-A; non-lethal; mutant; production; vaccine; protection; treatment; cancer; neutralising antibody; streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; group A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
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Pred. No. 3.9e-109;
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/label= sig_peptide
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Matches 247; Conservative
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Synthetic.
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non-lethal - used in vaccine composition for treatment of cancer and
streptococcal toxic shock syndrome etc.
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   Indels
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 Mismatches
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/label=_sig_peptide
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|abel= mat_peptide
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The present sequence is a non-lethal Streptococcus pyogenes Streptococcal toxin A (SPE-A) mutant, which can be used to produce vaccines to protect animals against wild type SPE-A and to treat cancer and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fascitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A can be selectively toxic to T cell lymphoma cells, N.B. Sequence not given in the specification, but
KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSN 240
                      Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine; protection; treatment; cancer; neutralising antibody; streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; group A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
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Pred. No. 1.7e-109;
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/label= sig_peptide
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/label= mat_peptide
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98.8%;
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                                                                                  TSQIEVYLITK 251
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Synthetic.
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                                                                                                           241 TSQIEVYLTTK
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181
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                                                                                                  Streptococcal; toxin A, SPE-A, non-lethal; mutant; production; vaccine; protection; treatment; cancer; neutraliaing antibody; streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; group A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
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                                                              Streptococcus pyogenes Streptococcal toxin A mutant Lysl6Asn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "wild type Lys replaced by Asn"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.6%; Score 1303; DB 2;
llarity 98.8%; Pred. No. 1.7e-109;
Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stoehr J,
                                                                                                                                                                                                                                                                                                                     1. .30
/label= sig_peptide
                                                                                                                                                                                                                                                                                                                                                                31. .251
/label= mat_peptide
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Synthetic.
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ses 248; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
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Peptide
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Matches
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6 8 6 8 6

Location/Qualifiers

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      Key
Peptide
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                                                                                                                                                                      The present sequence is a non-lethal Streptococcus pyogenes Streptococcal animals against mutant, which can be used to produce vaccines to protect animals against wild type SPE-A and to treat cancer and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fascitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A can be selectively toxic to T cell lymphoma cells. N.B. Sequence not given in the specification, but constructed using the wild type SPE-A sequence given on pages 77-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THENVKSVDQLLSHHLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSN 240
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                                                                                               Mutant SPB-A toxin with at least one amino acid change is substantially non-lethal - used in vaccine composition for treatment of cancer and streptococcal toxic shock syndrome etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine; protection; treatment; cancer; neutralising antibody; streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; group A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MENNKKVLKKMVPFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPV
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                                                                                                                                                                                                                                                                                                                                                                                                             1 MENNKKVLKKMVFFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPV
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                                                   Ohlendorf
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                                                                                                                                                                                                                                                                                                                                                            Score 1305; DB 2;
Pred. No. 1.1e-109;
1; Mismatches 2;
                                                   Stoehr J,
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                                                                                                                                                Example 4; Page; 102pp; English
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  95US-00480261
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Best Local Similarity 98.8
Matches 248; Conservative
                                                   Roggiani
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                        (MINU ) UNIV MINNESOTA
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Synthetic.
                                                                          WPI; 1997-099936/09.
                                                                                                                                                                                                                                                                                                                                     Sequence 251 AA;
                                                Schlievert PM,
07-JUN-1995;
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The present sequence is a non-lethal Streptococcus pyogenes Streptococcal toxin A (SPE-A) mutant, which can be used to produce vaccines to protect animals against wild type SPE-A and to treat cancer and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fascitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A can be selectively toxic to T cell lymphoma cells. N.B. Sequence not given in the specification, but constructed using the wild type SPE-A sequence given on pages 77-79
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                                                                                                                                                /note= "wild type Lys replaced by Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stoehr J, Ohlendorf D;
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Pred. No. 1.4e-109;
1; Mismatches 2;
.. .30
label= sig_peptide
                                                         31. .251
/label= mat_peptide
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nes 248; Conservative
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                                                                                                                   Misc-difference 187
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and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fascitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A can be electively toxic to T cell lymphoma cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New mutant Streptococcal SPE-A toxins - useful for, e.g. prevention or treatment of streptococcal infection or toxic shock syndrome.
                                                                                                                                                                                                                                                                                                                                                                                               KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSN
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                                                                                                                                                                                                                                                                                                                             ENAERSACIYGGVTNHEGNHLE1PKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVR
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPB-A toxin; nonlethal; mutant; Streptococcus pyogenes exotoxin A; wild type; nontoxic; antibody; vaccine; immunity; ovarian cancer; streptococcal toxic shock syndrome; STSS; T cell lymphoma;
                                                                                                                                                                                  ;
0
                                                                                                                                                      2; Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of Streptococcus pyogenes exotoxin A.
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                                                                                                                                                      Score 1308; DB 2;
Pred. No. 6e-110;
0; Mismatches 2
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Best Local Similarity
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                                                                                                                            Sequence 251 AA;
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This is the amino acid sequence of the Streptococcus pyogenes exotoxin A as change and is nonlethal compared with a protein to wild type SPE-A toxin. The novel mutant SPE-A toxins are noncoxin to wild type SPE-A toxins are nontoxic and can produce antibodies that neutralise wild type SPE-A toxins activity. The toxins can be used in vaccines and therapeutics to generate a protective immune response against streptococcal infection. They can be used to protect against the development of streptococcal toxic shock syndrome (STSS). In addition, streptococcal infection animals with symptoms of streptococcal infection and in methods for stimulating T cell proliferation and in the treatment of cancer. In particular they can be used for treating T cell lymphomas, and ovarian and uterine cancer
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                                                                                                                                                                                                                                                                                                                                          1 MENNKKYLKKAVFFVLVTFLGLTISQEVFAQQDPDFSQLHRSSLVKNLQNIYFLYEGDPV
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                                                                                                                                                                                                                                                   Length 251;
                                                                                                                                                                                                                                                  Score 1308; DB 2; Length 2
Pred. No. 6e-110;
0; Mismatches 2; Indels
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/label= sig_peptide
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/label= mat_peptide
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Matches 249; Conservative
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Synthetic.
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                                                                                                                                                                                                                      Sequence 251 AA;
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1.4e-110;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to treating a subject with cancer. The method involves administering an amount of a superantigen (SAg) composition comprising a molecule selected from: a native SAg protein; its biologically active fragment or a biologically active homologue or a biologically active fragment or a biologically active fragment or a biologically active fragment or biologically active fusion protein comprising the SAg or its fragment or biologically active fusion partner polypeptide or peptide. The SAg is selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic exotoxin, Y. pseudotuberculosis SAg, Mycoplasma arthritides SAg and Clostridium perfringens exotoxin. The method is useful in treating cancer or malignant diseases such as malignant pleural effusion, ascites, perioardial effusion or meningeal carcinomatosis. The present sequence represents a Streptococcal pyrogenic exotoxin A (SpEA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating a subject with cancer or malignant diseases comprises intratumoral, intrathecal or intracavitary administration of an amount a superantigen composition to the subject.
ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSPDIETNKKMVTAQELDYKVR
                                                                                                                                                                                                                                                                                                                                            enterotoxin, cytostatic, gene therapy, cancer, SpE; SpEA.
                                                                                                                                                                                                                                                                                                                    Streptococcal pyrogenic exotoxin A (SpEA) sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 16; 91pp; English
                                                                                                                                                                                                                                     ADF89839 standard; protein; 251 AA.
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2002US-0406637P.

2002US-0406750P.

2002US-0415310P.

2002US-0415310P.

2003US-0415400P.
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                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pyogenes,
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                                                                                                                                                                                                                                                                                                                                            Superantigen; SAg; e
pyrogenic exotoxin;
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15-JUN-2002;
28-AUG-2002;
29-AUG-2002;
01-OCT-2002;
02-OCT-2002;
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Length 251;

DB 8;

99.5%; Score 1315;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                substantially cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is Streptococcus pyogenes Streptococcal toxin A (S) -A), from which a non-lethal mutant SPE-A, comprising at least 1 amino acid change, can be derived. The mutant SPE-A can be used to produce vaccines to protect animals against wild type SPE-A and to treat cancer
                                                                                             61 THENVKSVDQLLSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC
                                                                                                                                                    ENAERSACIYGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKGAVVTAQELDYKVR
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                                                                             THENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC
                       1 MENNKKVLKKMVFFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPV
Gaps
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 Indels
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non-lethal - used in vaccine composition for treatment
streptococcal toxic shock syndrome etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                       pyogenes Streptococcal toxin A.
 Mismatches
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/label= mat_peptide
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 250; Conservative
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Protein Peptide

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fragment is altered so that binding of the encoded altered toxin DNA fragment is altered so that binding of the encoded altered toxin to ceither the MMC class II or T cell antigen receptor is altered. Also included are a recombinant DNA construct, postorion and an isolated and purified altered superantigen toxin DNA fragment), a host cell transformed with the recombinant DNA construct, producing altered superantigen toxin, an altered TSST-I (toxic shock syndrome toxin); superantigen toxin, an altered TSST-I (toxic shock syndrome toxin) or superantigen toxin peptide, diagnosing superantigen-associated bacterial for producing antigenic and immunogenic response resulting in the protection of amammal against superantigen-associated bacterial infection, an antisera isolated from individuals immunised with one or more altered TSST-I consension toxin and an antibody which recognises altered TSST-I consension toxin and an antibody which recognises altered TSST-I consension toxin and an antibody which recognises altered TSST-I consension toxin and an antibody which recognises altered TSST-I consension toxin and an antibody which recognises altered TSST-I composition for treating or preventing bacterial infection. The present sequence represents the L42A (with reference to the mature protein) content of SPEA. Note: The present sequence is not shown in the content of SPEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        superantigen toxin DNA fragment, useful for preparing a composition treating or preventing bacterial infection.
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                                                                                    SPEa, streptococcus pyrogenic enterotoxin a, mutant, vaccine, mutein, superantigen toxin; MHC; superantigen-associated bacterial infection; bacterial infection; antibacterial.
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Pred. No. 1.1e-110;
0; Mismatches 1;
                                         Streptococcus pyrogenic toxin a L42A mutant
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/label= Mature_SPEa_L42R
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/label= Signal_peptide
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27-AUG-2003 (first entry)
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Best Local Similarity
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                                                                                                                                                                         Streptococcus sp. Synthetic.
                                                                                                                                                                                                                                                                                                                                                     Misc-difference
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01-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention provides a superantigen toxin DNA fragment which has been genetically altered such that binding of the encoded altered toxin to either the MHC class II or T call antigen receptor is disrupted or altered. DNA fragments of the invention are useful in the production of vaccines against bacterial superantigen toxin infections. They are also useful in gene therapy. The present sequence is Streptococcus pyogenes pyrogenic exotoxin A (SpeA) protein. This sequence is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MENNKKVLKKMVFFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENAERSACI YGGVTNHEGNHLEI PKKI VVKVSI DGI QSLSFDI ETNKKMVTAQELDYKVR
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Superantigen toxin; vaccine; infection; pyrogenic exotoxin A; SpeA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                           1. .29
/label= Signal_peptide
30. .251
/note= "S. pyogenes mature SpeA protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1322; DB 7;
Pred. No. 3.3e-111;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                       (USME-) US MEDICAL RES INST INFECTIOUS DISEASES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Page 130-131; 141pp; English.
                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU62460 standard; protein; 251 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uvery match
Best Local Similarity 100.0%;
Matches 251; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                          26-NOV-2001; 2001US-00002784
                                                                                                                                                                                                                                                                                                                                26-NOV-2001; 2001WO-US046540
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                                                                  Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2003-492125/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAD56771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 251 AA;
                                                                                                                                                                                                                                         WO2003056015-A1
                      gene therapy
                                                                                                                                                                                                                                                                                     10-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ulrich RG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241
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The invention relates to an isolated and purified superantigen toxin DNA fragment is altered so that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is altered. Also included are a recombinant DNA construct (comprising a vector and an isolated and purified altered superantigen toxin DNA fragment), a host cell transformed with the recombinant DNA construct, producing altered superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin) superantigen toxin peptide, diagnosing superantigen-associated bacterial infection, a vaccine (comprising an altered superantigen toxin for producing antigenic and immunogenic response resulting in the protection of a mammal against superantigen-associated bacterial infection, an authority and immunogenic response dithone or more altered TSST-1 superantigen toxin and an antibody which recognises altered TSST-1. Superantigen toxin and an antibody which recognises altered TSST-1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA, SEB). The superantigen toxin DNA fragment is useful for preparing a composition for treating or preventing bacterial infection. The present composition for treating or preventing bacterial infection. The present contract of the mature protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Page 37-38; 68pp; English.
              97US-00882431.
98US-00144776.
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                                                                                                                                                     (ULRI/) ULRICH
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              25-JUN-1997;
                                                         01-SEP-1998;
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                                                                                                                                                                                                                                           Ulrich RG;
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                                                                                                                                      and/or DNA fragment, which has been altered so that the binding of the encoded toxin to either major histocompatibility complex (MHC) class II or T cell antigen receptor is altered. The superantigen toxins, DNA fragments, and vaccines are useful for treating or ameliorating superantigen-associated bacterial infection. The DNA fragments are particularly useful for producing vaccine against superantigen toxin infections. The transformed host cells are useful for analysing the effectiveness of drugs and agents that affect the binding of superantigens to MHC class II or T-cell antigen receptors. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSN
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                                                                                           invention relates to an isolated and purified superantigen toxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1322; DB 6;
100.0%; Pred. No. 3.3e-111;
ive 0; Mismatches 0;
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/label= Signal_peptide
    Claim 17; Page 34-35; 50pp; English.
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Matches 251; Conservative
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                                                                                                  MENNKKVLKKMVFFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPV
                                                           Gaps
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       Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pyogenes pyrogenic exotoxin A (SpeA) protein.
                                                      0, Indels
       100.0%; Score 1322; DB 7;
100.0%; Pred. No. 3.3e-111;
ive 0; Mismatches 0;
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Query Match
Best Local Similarity 100.0
Matches 251, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSQIEVYLTTK 251
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vaccine studies demonstrate that SPEa42 is highly antigenic, inducing protective immunity in a mouse animal model. The attenuated superantigen and beased to protect against superantigen toxin infections. Methods of producing and using altered superantigen toxins as vaccines, and in diagnosis and therapy, are provided by the invention. A multivalent excine consisting of altered superantigen toxins from SEA, SEB, SEC-1, TSST-1 and SPEa is predicted to provide protective immunity against the majority of bacterial superantigen toxins
                                                                                                                                                                                                                                                                                                                                                                             TSQIEVYLTTK
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OLSON M A.
                                                                                                                                               Local Similarity
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N-PSDB; ACA61184
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                                                                                                            Sequence 251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus
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                                                                                                                                   Query Match
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                                                                                                               MENNKKVLKKKVVFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated and purified superantigen toxin DNA fragment which has been genetically altered, useful for producing vaccine for treatment superantigen toxin-associated bacterial diseases.
                                                                                                1 MENNKKVLKKMVFFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPV
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                                                              3.3e-111;
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                                                   DB 3;
                                                                        0; Mismatches
                                                   Score 1322;
Pred. No. 3.
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ilarity 100.0%;
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                                                                                                                                                                                                                                                                                           TSQIEVYLTTK
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    bacterial infections
                                                             Similarity
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                          Sequence 251 AA;
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                                                                        Matches 251;
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                                        Gaps
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                              0
Length 251;
                                        Indels
  100.0%; Score 1322; DB 5; 100.0%; Pred. No. 3.3e-111;
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                                        0; Mismatches
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                                        Matches 251; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

September 17, 2005, 00:47:53; Search time 82.0376 Seconds (without alignments) 1183.322 Million cell updates/sec on:

Perfect score:

US-10-002-784A-16 1322 1 MENNKKVLKKWVFFVLVTFL......KDNFTLDSNTSQIEVYLTTK 251 Seguence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 Total number of hits satisfying chosen parameters:

2105692 seqs, 386760381 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* Geneseq 16Dec04:* geneseqp1990s:* geneseqp1980s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aay70109 Streptoco	Abb79508 Streptoco	Abul0088 Streptoco	Abu62331 Streptoco	Aae37683 Streptoco	Abu62460 Streptoco	Adf89839 Streptoco	Aaw12097 Streptoco	Aaw59780 Amino aci	Aaw12154 Streptoco	Aaw12146 Streptoco	Aaw12150 Streptoco	Aaw12147 Streptoco	Aaw12148 Streptoco	Aaw12153 Streptoco	Aaw12151 Streptoco	Aaw12152 Streptoco		Aaw12145 Streptoco	Aaw59798 Amino aci	Aaw59781 Amino aci	Aab67344 Streptoco	Aar13209 Streptoco	Aar45017 Staphyloc	Abb76240 Staphyloc
. QI	AAY70109	ABB79508	ABU10088	ABU62331	AAE37683	ABU62460	ADF89839	AAW12097	AAW59780	AAW12154	AAW12146	AAW12150	AAW12147	AAW12148	AAW12153	AAW12151	AAW12152	AAW12149	AAW12145	AAW59798	AAW59781	AAB67344	AAR13209	AAR45017	ABB76240
DB	16	'n	9	7	7	7	ထ	~	~	N	~	N	7	~	N	~	~	~	7	7	7	4	~	N	ហ
% Query Match Length	251	251	251	251	251	251	251	251	251	251	251	251	251	251	251	251	251	251	250	251	251	221	221	221	221
* Query Match	100.0	100.0	100.0	100.0	100.0	99.5	99.5	98.9	98.9	98.7	98.6	98.6	98.6	98.3	98.2	98.2	98.2	97.8	97.5	97.4	97.3	88.5	æ	88.0	88.0
Score	1322	1322	1322	1322	1322	1316	1315	1308	1308	1305	1304	1303	1303	1299	1298	1298	1298	1293	1288.5	1288	1286	1170	1164	1164	1164
Result No.	-	7	٣	4	2	ø	7	80	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Abu62334 Streptoco	Aae37687 Streptoco	Abu62335 SPEa L42R	Aae37684 Streptoco	Aae37689 S. pyogen	Aae37688 S. pyogen	Aae37691 S. pyogen	Abu79074 S. pyogen	Adf43300 Pyrogenic	Aaw06737 Staphyloc	Abu79069 S. aureus	Abg75015 S aureus	Adf43290 Staphyloc	Aaw64647 Synthetic		Abu62454 S. aureus	Adf89825 Staphyloc	Aab67341 Staphyloc	Abg75016 Unidentif	_
ABU62334	AAE37687	ABU62335	AAE37684	AAE37689	AAE37688	AAE37691	ABU79074	ADF43300	AAW06737	ABU79069	ABG75015	ADF43290	AAW64647	AAY92319	ABU62454	ADF89825	AAB67341	ABG75016	ADL14247
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220	220	468	468	220	220	468	250	250	255	266	566	266	239	266	266	238	239	239	239
85.9	85.9	85.9	85.9	92.6	85.5	85.5	81.4	81.4	44.5	43.6	43.6	43.6	43.6	43.5	43.5	43.4	43.4	43.4	43.4
1136	1136						1075.5		288	576.5		576.5		575	574.5	574	574	574	574
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ดั	7	Ñ	Ñ	m	m	m	m	m	m	m	m	m	m	4	4	4	4	4	4

ALIGNMENTS

Streptococcal pyrogenic exotoxin A (SPE-A). AAY70109 standard; protein; 251 AA. (first entry) 05-JUN-2000 AAY70109; AAY70109
AAY

Superantigen toxin; SAg; Streptococcal pyrogenic exotoxin A; SPE-A; antibacterial; vaccine; MRC class II receptor; T-cell antigen receptor; cytostatic; antibody; staphylococcal/streptococcal toxin; toxxid; SPEA42; diagnosis; treatment; superantigen-associated bacterial infection.

Streptococcus sp.

WO200009154-A1.

24-FEB-2000.

98WO-US016766. 13-AUG-1998; 98WO-US016766. 13-AUG-1998; (REED-) REED ARMY INST RES WALTER.

Bavari S; Olson MA, Ulrich RG,

WPI; 2000-224177/19.

N-PSDB; AAZ51112.

Nucleic acid encoding superantigen toxin useful as a vaccine and for diagnosis of superantigen-associated bacterial infections.

Example 12; Page 94-95; 118pp; English.

The present amino acid sequence is the Streptococcal pyrogenic exotoxin A (SPE-A), a bacterial superantigen toxin (SAg), used for the formulation of SPE-A vaccine SPEA42. The coding region of this SAg toxin is altered by site directed mutagenesis, introducing L42R mutation, that results in disruption of binding of the toxin to both the MHC class II or T-cell antigen receptor. SPE-A has antibacterial and cytostatic activity. This sequence is useful for the production of SPE-A vaccines and specific antibodies. This vaccine overcomes the disadvantages of the chemically inactivated toxoids and is designed to protect individuals against one or several related staphylococcal and streptococcal toxins. It is used for the diagnosis and treatment or amelioration of superantigen-associated